





RESULT 7  
 S51364 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
 spm1 -til-specific protein mst101(2) - fruit fly (*Drosophila hydei*)  
 C;Species: *Drosophila hydei*  
 C;Date: 19-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
 C;Accession: S51364; S34154  
 R;Neesen, J.; Padmanabhan, S.; Buenemann, H.  
 Eur. J. Biochem. 225, 1089-1095, 1994  
 A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represses  
 alpha-helical rods within the extremely elongated spermatozoa of *Drosophila hydei*.  
 A;Reference number: S51364; MUID:9505538; PMID:795719  
 A;Accession: S51364  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 1-1390 <NEW>  
 A;Cross-references: EMBL:X73481  
 R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.  
 submitted to the EMBL Data Library, June 1993  
 A;Reference number: S34153  
 A;Accession: S34154  
 A;Molecule type: DNA  
 A;Residues: 1-163, 'B', 164-236, 'Q', 237-254, 257-320, 'E', 321-1390 <NEW>  
 A;Cross-references: EMBL:X73481; NID:9313101; PID:313202  
 C;Genetics:  
 A;Gene: mst101(2)  
 A;Cross-references: FlyBase:FBgn0011816  

Query Match 42.3%; Score 90; DB 2; Length 1390;  
 Best Local Similarity 57.8%; Pred. No. 0.41; Mismatches 11; Indels 4; Gaps 2;  
 Matches 26; Conservative 4; A;Residues: 1-163, 'B', 164-236, 'Q', 237-254, 257-320, 'E', 321-1390 <NEW>  
 QY 2 KKVAKKAKKE-AKKAYKAEEAKK---AKKYYAAEKKAEEAKKAEEAYEA 42  
 DB 662 KETPKKKC-KEAKKKEAEEAKKEAEEAKKKC-HEA 706

RESULT 8  
 A28100 B87553  
 histone H1-beta, embryonic - sea urchin (*Strongylocentrotus purpuratus*)  
 C;Species: Strongylocentrotus purpuratus (purple urchin)  
 C;Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 23-Feb-1997  
 C;Accession: A28100  
 R;Lai, Z.C.; Childs, G.  
 Mol. Cell. Biol. 8, 1842-1844, 1988  
 A;Title: Characterization of the structure and transcriptional patterns of the gene encoding histone H1.  
 A;Reference number: A28100; MUID:88246461; PMID:2837660  
 A;Accession: A28100  
 A;Molecule type: DNA  
 A;Residues: 1-211 <LAI>  
 A;Cross-references: GB:M20314  
 C;Keywords: histone H1  
 C;Superfamily: chromosomal protein; DNA binding; embryo; nucleosome; nucleus  

Query Match 42.0%; Score 89.5; DB 2; Length 211;  
 Best Local Similarity 61.9%; Pred. No. 0.01; Mismatches 26; Conservative 3; Indels 10; Gaps 2;  
 Matches 26; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 1 AKKYAKKAKKEAKKAKKAEEAKKAKKEAEEAKKAEEAYEA 42  
 DB 139 SKKTTKKYKKPAAKKAKKEA-ACKRAK--KPAKKPKAKKA 177

RESULT 9  
 G70673 B43592  
 probable hupB - *Mycobacterium tuberculosis* (strain H37RV)  
 C;Species: *Mycobacterium tuberculosis*  
 C;Accession: G70673  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feilwell, T.; Gentle, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

RESULT 10  
 B87553  
 DNA topoisomerase I [imported] - *Caulobacter crescentus*  
 C;Species: *Caulobacter crescentus*  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C;Accession: B87553  
 R;Nierman, W.C.; Falblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Daub, M.T.; DeBoy, R.T.; Dobson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolodkin, J.; Ermolava, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-899 <STO>  
 A;Cross-references: GB:AB005673; NID:913423998; PIDN:AAK24422.1; GSDB:GN00148  
 C;Genetics:  
 A;Gene: CC2451  
 C;Superfamily: bacterial type I DNA topoisomerase  

Query Match 41.3%; Score 88; DB 2; Length 899;  
 Best Local Similarity 58.7%; Pred. No. 0.45; Mismatches 27; Conservative 5; Indels 12; Gaps 2; Matches 27; Conservative 5; Mismatches 12; Indels 2; Gaps 2;

QY 1 AKKYAKKAKKEAKKAKKAEEAKKAKKEAEEAKKAEEAYEA 42  
 DB 836 AKKPAAKAAATSKAKAKESDAPAKTAA-KKPAAKPKAKKA 880

RESULT 11  
 B43592  
 outer membrane protein TmpB - *Treponema phagedenis*  
 C;Species: *Treponema phagedenis*  
 C;Date: 30-Jan-1993 #sequence\_revision 12-Mar-1993 #text\_change 08-Oct-1999  
 C;Accession: B43592  
 R;Relton, D.B.; Limberger, R.J.; Curci, R.; Malinosky-Rummell, P.; Slivinski, L.; Schon, Infect. Immun. 59, 3685-3693, 1991  
 A;Title: Treponema phagedenis encodes and expresses homologs of the *Treponema pallidum* A;Reference number: A43592; MUID:91372983; PMID:1894368  
 A;Accession: B43592  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-384 <IEL>  
 A;Cross-references: C;Keywords: membrane protein  

Query Match 40.6%; Score 86.5; DB 2; Length 384;  
 Best Local Similarity 54.5%; Pred. No. 0.32; Mismatches 24; Conservative 6; Indels 1; Gaps 1;

RESULT 12

F70742 hypothetical protein Rv0475 - *Mycobacterium tuberculosis* (strain H37Rv)

C;Species: *Mycobacterium tuberculosis*  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C;Accession: F70742  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Churchar, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feitwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Roberts, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
A;Reference number: A70500; MUID: 9829587; PMID: 9634230  
A;Accession: F70742  
A;Status: preliminary; nucleic acid sequence not shown;  
A;Molecule type: DNA  
A;Residues: 1-199 <COL>  
A;Cross-references: GB:Z77162; GB:AL123456; NID:93261605; PIDN:CAR00936.1; PID:9255021;  
A;Experimental source: strain H37Rv  
C;Genetics: Rv0475

Query Match Score 86; DB 2; Length 199;  
Best Local Similarity 65.6%; Pred. No. 0.21; Mismatches 4; Indels 0; Gaps 0;  
Matches 21; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 11 EKAKKAKAKAAEAKKAKAKYKEKAEEAKKAKAA 42  
Db 161 KKAAPAKKAAPAKKAAPAKKAAPAKKA 192

RESULT 13

S34153 mst101-1 protein - fruit fly (*Drosophila hydei*)  
C;Species: *Drosophila hydei*  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S34153  
R;Neszen, J.; Hainlein, U.A.O.; Bueemann, H.  
A;Reference number: S34153  
A;Accession: S34153  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-344 <NL>  
A;Cross-references: EMBL:X73480; NID:9313199; PID:9313200  
A;Gene: FlyBase:Dhyd/mst101  
A;Cross-references: FlyBase:FBgn0011816  
C;Superfamily: neurofilament triplet H protein

Query Match Score 86; DB 2; Length 199;  
Best Local Similarity 57.8%; Pred. No. 0.33; Mismatches 3; Indels 4; Gaps 2;  
Matches 26; Conservative 3; Mismatches 12; Indels 4; Gaps 2;

QY 2 KKAKKAK-AEKAKKAKAKAAEAKK--AAKYKEKAEEAKKAKAA 42  
Db 69 KKAEEKKCAEAKKEKEAEKKCAEAKKEKEAEKKCAAA 113

RESULT 14

E83525 Iota Protein PA0571 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C;Species: *Pseudomonas aeruginosa*  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: E83525  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradmin, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83525  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residue: 1-347 <STO>  
A;Cross-references: GB:AE04530; GB:AE004091; NID:9946865; PIDN:AG04360.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: tolA; PA0971

Query Match Score 86; DB 2; Length 347;  
Best Local Similarity 51.1%; Pred. No. 0.33; Mismatches 6; Indels 2; Gaps 1;  
Matches 24; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

QY 1 AKYVAKKAKAEGAKKA-YKAAEAKKAKAKYKEKAEEAKKAYEA 45  
Db 125 AKKAEEAKKAKDAEKKAAEAKKAEQKKQADIAKRADEEAKKKAAEDA 171

RESULT 15

S61925 histone H1 homolog - *Bordetella pertussis*  
C;Species: *Bordetella pertussis*  
C;Date: 23-Jul-1995 #sequence\_revision 06-Sep-1996 #text\_change 24-Nov-1999  
C;Accession: S61926; S69327  
R;Scariato, V.; Arico, B.; Goyard, S.; Ricci, S.; Manetti, R.; Prugnola, A.; Manetti, R.  
A;Title: A novel chromatin-forming histone H1 homologue is encoded by a dispensable and  
A;Reference number: S61926; MUID:95319329; PMID:7596289  
A;Accession: S61926  
A;Molecule type: DNA  
A;Residues: 1-182 <SCA1>  
A;Cross-references: EMBL:1137438; NID:977717; PIDN:AAB59120.1; PID:977718  
A;Accession: S63327  
A;Molecule type: protein  
A;Residues: 'X'; 3-39 <SCA2>  
C;Genetics:  
A;Gene: bphI

Query Match Score 85; DB 2; Length 182;  
Best Local Similarity 61.4%; Pred. No. 0.25; Mismatches 9; Indels 4; Gaps 3;  
Matches 27; Conservative 4; Mismatches 9; Indels 4; Gaps 3;

QY 1 AKYVAKKAKAET--AKYV-KAAEAKKAKAKYKEKAEEAKKAA 41  
Db 58 AKVAKAKAVAKAVAKAVAKAVAKAVAKAVAKAVAKAVAK 100

Search completed: April 20, 2004, 23:18:23  
Job time : 8.88961 secs

OM protein - protein search, using sw model  
Run on: April 20, 2004, 23:14:00 ; Search time 9.35065 Seconds  
Perfect score: 213 ; (without alignments)  
Sequence: 1 AKYAKAKAEEKKAKKAYAA.....AKYEKAEEKAEEKAAYEA 45  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: US-09-816-989A-2  
US-09-816-989A-2  
1 AKYAKAKAEEKKAKKAYAA.....AKYEKAEEKAEEKAAYEA 45  
BLOSUM62  
Gapop 10.0 , Gapext 0.5  
389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
listing first 45 summaries

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 4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:  
 5: /cgn2\_6/prodata/2/iaa/PCTTUS\_COMB.pep:  
 6: /cgn2\_6/prodata/2/iaa/backfile1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match Length	DB ID	Description
1	213	100.0	45	4	US-09-405-743A-2
2	138	64.8	109	4	US-09-405-743A-7
3	134.5	63.1	56	4	US-09-405-743A-3
4	131	61.5	77	4	US-09-405-743A-5
5	126.5	59.4	86	4	US-09-405-743A-6
6	108	56.6	66	4	US-09-405-743A-4
7	50.7	35	4	US-09-405-743A-1	
8	91	44.6	469	4	US-09-489-039A-13565
9	91	42.7	223	4	US-09-485-855-201
10	91	42.7	223	4	US-09-205-426-201
11	89.5	42.0	214	3	US-09-041-889-27
12	89.5	42.0	214	4	US-09-17-264-27
13	85	40.4	407	4	US-09-252-991A-29581
14	81.5	38.3	497	4	US-09-134-000C-5990
15	78	36.6	316	4	US-09-252-991A-322957
16	77.5	36.4	700	4	US-09-107-532A-5094
17	77	36.2	103	3	US-09-041-889-9
18	77	36.2	103	4	US-09-417-264-39
19	77	36.2	116	3	US-09-041-889-38
20	77	36.2	116	4	US-09-417-264-38
21	77	36.2	158	3	US-09-041-889-40
22	77	36.2	158	4	US-09-417-264-40
23	77	36.2	222	3	US-09-041-889-3
24	77	36.2	222	3	US-08-8337-058-3
25	77	36.2	222	4	US-09-417-264-3
26	77	36.2	226	3	US-09-041-889-3
27	77	36.2	226	4	US-09-417-264-32

**ALIGNMENTS**

```

RESULT 1
US-09-05-743A-2
; Sequence 2, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09-405-743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPIDE

US-09-405-743A-2
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Best Local Similarity 100.0%; Pred. No. 1.4e-16; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0; Sequence 1, Appli
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; RESULT 2
US-09-05-743A-7
; Sequence 7, Application US/09405743A
; Sequence 27, Appli
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09-405-743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
; US-09-05-743A-7

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CURRENT APPLICATION NUMBER: US/09/405,743A  
 CURRENT FILING DATE: 1999-09-24  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn Ver. 2.1  
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 LENGTH: 35  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: SYNTETIC  
 OTHER INFORMATION: Peptide  
 US-09-405-743A-1

Query Match Similarity 50.7%; Score 108; DB 4; Length 35;  
 Best Local Similarity 64.4%; Pred. No. 1.7e-05; Mismatches 5; Indels 10; Gaps 2;  
 Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

QY 1 AKKYAKKAKAKKAKYKAEEAKKAKYKAAKEAAKEAYEA 45  
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RESULT 8

US-09-489-039A-13565  
 Sequence 13565, Application US/09489039A  
 Patent No. 6610836  
 GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al.  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 2705\_200401  
 CURRENT APPLICATION NUMBER: US/09/489,039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117,747  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO 13565  
 LENGTH: 469  
 TYPE: PRT  
 ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-13565

Query Match Similarity 44.6%; Score 95; DB 4; Length 469;  
 Best Local Similarity 52.9%; Pred. No. 0.006; Mismatches 14; Indels 6; Gaps 1;  
 Matches 27; Conservative 4; Mismatches 14; Indels 6; Gaps 1;

QY 1 AKKYAKKAKAKKAKYKAEEAKKAKYKAAKEAAKEAYEA 45  
 Db 242 AAEOKKAKAAKKAQOEAKKAQOEAKKAQAAKEAKKAQAAKEAKKAQKA 292

RESULT 9

US-09-095-855-201  
 Sequence 201, Application US/09095855  
 Patent No. 6160093  
 GENERAL INFORMATION:  
 APPLICANT: Tan, Paul  
 APPLICANT: Visser, Elizabeth  
 APPLICANT: Skinner, Margot  
 APPLICANT: Prestidge, Ross  
 TITLE OF INVENTION: Compounds and Methods for Treatment and Diagnosis of Mycobacterial Infections  
 FILE REFERENCE: 11000\_1002c4  
 CURRENT APPLICATION NUMBER: US/09/205,426  
 CURRENT FILING DATE: 1998-12-04  
 EARLIER APPLICATION NUMBER: 07/095,855  
 EARLIER FILING DATE: 1998-06-11  
 EARLIER APPLICATION NUMBER: 08/997,362  
 EARLIER FILING DATE: 1997-12-22  
 EARLIER APPLICATION NUMBER: 08/873,970  
 EARLIER FILING DATE: 1997-06-12  
 EARLIER APPLICATION NUMBER: 08/1705,347  
 EARLIER FILING DATE: 1996-08-29  
 NUMBER OF SEQ ID NOS: 208  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 201  
 LENGTH: 223  
 TYPE: PRT  
 ORGANISM: Mycobacterium vaccae  
 US-09-205-426-201

Query Match Similarity 42.7%; Score 91; DB 4; Length 223;  
 Best Local Similarity 59.6%; Pred. No. 0.0074; Mismatches 12; Indels 2; Gaps 2;  
 Matches 28; Conservative 5; Mismatches 12; Indels 2; Gaps 2;

QY 1 AKYA-KAKAKAKAKKAKYKAEEAKKAKYKAAKEAAKEAYEA 45

RESULT 11  
 US-09-041-889-27  
 ; Sequence 27, Application US/09041889  
 ; Patent No. 6033864  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Braun, Jonathan  
 ; APPLICANT: Colavvy, Offer  
 ; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative Coilitis, and Clinical Subtypes Thereof, Using Title of Invention: Microbial UC PANCA antigens  
 ; NUMBER OF SEQUENCES: 41  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell & Flores LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/041,889  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 09/041,889  
 ; FILING DATE: 11-APR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-FM 3006  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 27:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 214 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: peptide  
 ; US-09-0417-264-27  
 ;  
 Query Match 42.0%; Score 89.5; DB 4; Length 214;  
 Best Local Similarity 55.6%; Pred. No. 0.01; Pred. No. 0.01;  
 Matches 25; Conservative 13; Indels 3; Gaps 1;  
 QY 1 AKKYAKKAKAEEKAKKAYKAEEKAKKAYKEKAEEKAKEAYEA 45  
 Db 111 AKKVAKKAPAKKATKAKKATKAPKA--RKAAKTRPAKAKATA 152  
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 RESULT 13  
 US-09-252-991A-29581  
 ; Sequence 2981, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenstein et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITIUS FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO: 29581  
 ; LENGTH: 407  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-29581  
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 Query Match 40.4%; Score 86; DB 4; Length 407;  
 Best Local Similarity 51.1%; Pred. No. 0.047; Mismatches 15; Indels 2; Gaps 1;  
 Matches 24; Conservative 6; Mismatches 15; Indels 2; Gaps 1;  
 QY 1 AKKYAKKAKAEEKAKKAYKAEEKAKKAYKEKAEEKAKEAYEA 45  
 Db 185 AKQAKAKAKDDEBKEZAEKZAEQKQDADTAKRABEAKKKAKDA 231  
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 RESULT 14  
 US-09-134-000C-5990  
 ; Sequence 5990, Application US/09134000C  
 ; Patent No. 6617156

; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032196-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5990  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis\_B  
; US-09-134-000C-5990

Query Match 38.3%; Score 81.5; DB 4; Length 497;  
Best Local Similarity 47.1%; Pred. No. 0.17; Mismatches 7; Indels 7; Gaps 1;  
Matches 24; Conservative 7; MisMatches 13; Del 7; Gap 1;

Qy	2	KRYAKKAKAK-----AKKAYKAKAKYKAQAAQQAQAAEQAQATAANEA	45
Db	236	KKEAEKRLAEEQARQRAAKKAAEQAAQQAQAAEQAQATAANEA	286

RESULT 15  
US 09-252-991A-32957  
; Sequence 32957, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 33142  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-32957

Query Match 36.6%; Score 78; DB 4; Length 316;  
Best Local Similarity 54.8%; Pred. No. 0.26; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0; MisMatches 19; Del 0; Gap 0;

Qy	1	AKKYAKKAKAKAKYKAQAAKQAKYKAQAAKAKAAKEAA	42
Db	157	AKAAKKPAAKPAAKPAKTAQAAKCPAKPAKAAKPKAA	198

Search completed: April 20, 2004, 23:19:07  
Job time : 9.35065 secs







Db	Qy	1 AKKAKOAKAEGKKAKKAEEKKAKKAKKEAKALAKALEAYEA 45 111 AKVAKAPAKATKAACKAATKAPA--RKATKAPAKATKA 152
RESULT 6	DBH_MYCB	DBH MYCB
ID	DBH MYCB	STANDARD; PRT; 214 AA.
AC	Q9XB8; Q9S5J5; 1;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	15-MAR-2004 (Rel. 43, Last sequence update)	
DE	DNA-binding protein HU homolog (Histone-like protein) (Hlp).	
DE	HUP OR HLP OR RUPB OR MDPI OR MB3010C.	
OS	Mycobacterium bovis.	
OC	Bacteria; Actinobacteria; Actinomycetales;	
OC	Corynebacteriales; Nocardioides; Nocardioidales;	
OC	NCBI_TaxID=1765;	
RP	SEQUENCE FROM N.A.	
RC	PRABHAKAR S., Tyagi J.S., Prasad H.K.,	
RA	"HlpB-A target for differentiation of <i>M. tuberculosis</i> and <i>M. bovis</i> .";	
RT	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RL	[1] -	
RN	SEQUENCE FROM N.A.	
RA	STRAIN=BCG / Tokutake H., Matsuo T., Mineya T., Yamada T.,	
RA	Matsumoto S., Yukitake H., Matsuo T., Mineya T., Yamada T.,	
RT	"Identification of a novel protein generating bacterial slow growth	
RT	from Mycobacterium.", Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.	
RL	[3]	
RN	SEQUENCE FROM N.A.	
RA	STRAIN=AF2122197;	
RA	GARNIER T., BISGMEIER K., CAMUS J.-C., MEDINA N., MANSOOR H.,	
RA	PRIYOR M., DUTTIGY S., GRODIN S., LACROIX C., MONSEMPPE C., SIMON S.,	
RA	HARRIS B., ATKIN R., DOGETT J., MAYES R., KATING L., WHEELER P.R.,	
RA	HARRIS B., ATKIN R., DOGETT J., MAYES R., KATING L., WHEELER P.R.,	
RA	PARKILL J., BARRELL B.G., COLE S.V., HEWINSON R.G.,	
RA	"The complete genome sequence of <i>Mycobacterium bovis</i> .";	
RA	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).	
-!- FUNCTION: Histone-like DNA-binding protein which is capable of		
-!- wrapping DNA to stabilize it, and thus to prevent its denaturation		
-!- under extreme environmental conditions (By similarity).		
-!- SIMILARITY: Belongs to the bacterial histone-like protein family.		
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or send an email to license@isb-sib.ch).		
CC	SEQUENCE FROM N.A.	
RA	STRAIN=H37Rv;	
RA	COLE S.T., BROSCHE R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,	
RA	GORDON S.V., BISGMEIER K., COLE S.V., BARRY C.E. III, TEKIA F.,	
RA	BRADCOCK K., BASIM D., BROWN D., CHILLINGWORTH T., CONNOR R.,	
RA	DAVIES R., DEVLIN K., FEWTWELL T., GENTILES S., HAMLIN N., HOLROYD S.,	
RA	HORNBY T., JAGELS K., KROHN A., MCLEAN J., MOULE S., MURPHY L.,	
RA	OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,	
RA	RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQUARES R.,	
RA	SULSTON J.B., TAYLOR K., WHITEHEAD S., BARRELL B.G.,	
RT	"Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the	
RT	complete genome sequence.",	
RL	Nature 393:537-544 (1998).	
RN	SEQUENCE OF 71-86, AND DNA-BINDING.	
RC	STRAIN=R37Av;	
RA	PRASAD H.K., ANNAPURNA P.S., DEY A.B., TYAGI J.S., JAIN N.K.,	
RA	SAVITA P.,	
RL	Submitted (DEC-1997) to Swiss-Prot.	
CC	-!- FUNCTION: Histone-like DNA-binding protein which is capable of	
CC	wrapping DNA to stabilize it, and thus to prevent its denaturation	
CC	-!- under extreme environmental conditions (By similarity).	
CC	-!- SIMILARITY: Belongs to the bacterial histone-like protein family.	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
CC	or send an email to license@isb-sib.ch).	
DR	EMBL; AB01421; CAB4493.1; -.	
DR	EMBL; BX48341; CAD96697.1; -.	
DR	HSPP; P02346; IHUU.	
DR	INTERPRO; IPR000119; Bac_DNAbind.	
DR	PIANT; PFO0216; Bac_DNA_bind; 1.	
DR	PRINTS; PR01727; DNABINDINGHO.	
DR	PRODOM; PD00045; Bac_DNAbind; 1.	
DR	SMART; SM00411; BH1; 1.	
DR	PROSITE; PS00045; HISTONE-LIKE; 1.	
DR	DNA-binding; DNA condensation; Repeat; Complete proteome.	
FT	DOMAIN 1 214 BACTERIAL HISTONE-LIKE DOMAIN.	
FT	DOMAIN 1 90 DEGENERATE REPEATS REGION.	
FT	101 214 MISSING (IN REF. 1 AND 2).	
FT	137 145 MISSING (IN REF. 1 AND 2).	
FT	CONFLICT 208 208 T->A (IN REF. 1).	
FT	SEQUENCE 214 AA; 22187 MW; CB09AF20FB353544 CRC64;	
Query Match	42.0%; Score 89.5; DB 1; Length 214;	
Best Local Similarity	55.6%; Pred. 0.025; 13; Indels 3; Gaps 1;	
Matches	25; Conservative 4; Mismatches	





CC -!- DOMAIN: HEPARIN BINDING SEEMS TO REQUIRE THE C-TERMINAL END  
 CC DOMAIN OF HBHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL END  
 CC DIMINISH THE AFFINITY FOR HEPARIN.  
 CC -!- PTM: GLYCOSYLATED. GLYCOSYLATION MAY PROTECT THE PROTEIN FROM  
 CC PROTEOLYTIC DEGRADATION AND BE IMPORTANT FOR HEMAGGLUTINATION. IT  
 CC SUGGESTS THAT THE CARBOHYDRATE MOIETY MAY BE LOCATED WITHIN THE C-  
 CC TERMINAL DOMAIN OF HBHA.  
 CC -!- MISCELLANEOUS: SERUM FROM PATIENTS DIAGNOSED WITH ACTIVE  
 CC TUBERCULOSIS THAT HAD NOT BEEN VACCINATED CONTAINS ANTIBODIES THAT  
 CC RECOGNIZE HBHA, WHEREAS SERUM FROM HEALTHY INDIVIDUALS DOES NOT  
 CC CONTAIN ANY.  
 CC -!- SIMILARITY: STRONG, TO M. LEPRAE HBHA.

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 CC or send an email to license@isb-sib.ch).

CC DR EMBL; X74480; CAA53875.1;  
 CC DR PIR; S34153; S34153.  
 CC DR FLYBase; FBgn0011810; Dhydmat101(1).  
 CC DR GO; GO:0005737; C:cytoplasm; IDA.  
 CC DR GO; GO:0005198; F:structural molecule activity; IEP.  
 CC DR GO; GO:007288; P:axoneme assembly; IEP.  
 CC DR Sperm; Repeat; Multigene family.  
 CC FT DOMAIN 58 337 19 X 16 AA APPROXIMATE TANDEM REPEATS OF  
 CC SQ PIR; K-K-R-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X.  
 CC FT PIR; 24C65D2510387E2A CRC64;  
 CC SQ SEQUENCE 344 AA; 37793 MW; 24C65D2510387E2A CRC64;  
 CC FT Query Match 40 4%; Score 86; DB 1; Length 344;  
 CC DR Best Local Similarity 57.8%; Pred. No. 0.084;  
 CC DR Matches 26; Conservative 3; Mismatches 12; Indels 4; Gaps 2;  
 CC DR Qy 2 KRYAKAK-ABKAKAYKAEEAKK--AAYKEAKAAEKAKAA 42  
 CC DR Db 69 KEAAEKKCABAKEKEKAEEKKCAEAKKEKEKAEEKKCAEA 113  
 CC  
 RESULT 12  
 MSLT1\_DROGY ID MSLT1\_DROGY STANDARD; PRT; 344 AA.  
 AC Q08635; DT 01-FEB-1995 (Rel. 31, Created)  
 DT 15-Mar-2004 (Rel. 43, last annotation update)  
 DE Axoneme-associated protein mstl01(1).  
 GN MSTL01(1);  
 OS Drosophila hydei (Fruit fly).  
 OC Buraryana; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Epdyroidea; Drosophilidae; Drosophila;  
 OX NCBI\_TaxID=7244;  
 RN [1] RPT  
 SEQUENCE FROM N.A.  
 RN STRAIN=PACO;  
 RN  
 RESULT 13  
 TOLA\_PSEAE ID TOLA\_PSEAE STANDARD; PRT; 347 AA.  
 AC P50600; DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DE TOLA Protein.  
 GN TOLA OR PA0971.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OK NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=PACO;  
 RP MEDLINE=97113525; PubMed=8955385;  
 RA Dennis J.J., Lafontaine E.R., Sokol P.A.;  
 RA "Identification and characterization of the tolQRA genes of  
 RT Pseudomonas aeruginosa";  
 RT J. Bacteriol. 178:7059-7068(1996).  
 RN [2]  
 RP REVISIONS TO N-TERMINUS.  
 RA Duan K., Sokol P.A.;  
 RA Submitted (AUG-1999) to the EMBL/GenBank/DDJB databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=ATCC\_15692 / PA01;  
 RP MEDLINE=2043737; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.J., Mizoguchi S.D., Warrener P.,  
 RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltz L., Tolentino E., Westbroek-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith R.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen";  
 RL Nature 406:950-954(2000).  
 CC -!- FUNCTION: Involved in the tonB-independent uptake of proteins (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane  
 CC (Potential).

CC -!- DOMAIN: The predominant structure is alpha-helical.



GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: April 20, 2004, 23:12:24 ; Search time 21.039 Seconds  
674.858 Million cell updates/sec

Title: US-09-816-989a-2

Perfect score: 213

Sequence: I AKKYAKKAKAEKAKKAYKA.....AKYEKAAEKAKEAYEA 45

Scoring table: BLOSUM62

Gapop 1.0 . Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

**Database :**

- 1: SPTREMBL\_25,\*
- 2: sp\_archae:\*
- 3: sp\_bacteria:\*
- 4: sp\_fungi:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacterian:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Match Length	DB ID	Query	Description
1	108.5	50.9	379	16	Q7WFNS
2	103.5	48.6	373	16	Q7WFNS
3	98.5	46.2	461	16	Q7WB4
4	98	46.0	394	16	Q8X655
5	98	46.0	421	16	Q8F0T1
6	95	44.6	413	16	Q83SA1
7	94.5	44.4	239	16	Q8Y5W4
8	93.5	43.9	248	16	Q81H69
9	92	43.2	117	16	Q89dA0
10	91	42.7	244	16	Q9AUX2
11	90.5	42.5	197	16	Q7w3X2
12	90	42.3	243	16	Q92A67
13	89	41.8	182	2	Q8RL16
14	88.5	41.5	372	2	Q9wmX1
15	88.5	41.5	372	16	Q88n16
16	41.3	225			Q7WFa2

RP SEQUENCE FROM N.A.  
RC STRAIN=RB50 / ATCC BAA-588;  
RX MEDLINE=22827954; Pubmed=12910271;  
RA Parkhill J., Seabright M., Preston A., Murphy L.D., Thomson N., Mungall K.L.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cardeno-Tirrago A.M., Temple L., James K., Harris R., Quail M.A.,  
RA Achtmann M., Atkin R., Baker S., Basham D., Basson N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moile S., Norberczak H., O'Neill S., Ormond D., Price C.,  
RA Rabbinkowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin J., Whitehead S., Barrill B.G., Maskell D.J.;  
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,  
*Bordetella parapertussis* and *Bordetella bronchiseptica*.";  
RL Nat. Genet. 35:32-40 (2003);  
DR EMBL: BX60449; CAB34600.1; -.

RW SEQUENCER 379 AA; 40776 MW; C657B5AEE97BDD3 CRC64;

Query Match 50.9%; Score 108.5; DB 16; Length 379;  
Best Local Similarity 65.1%; Pred. No. 0.0043; Matches 28; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

OY 5 AKKAKAKKAKKAKAEEKKAKAYK---KAEEKAKEAYEA 44







OS Listeria innocua.  
 OC Bacteria; Fimicutes; Bacillales; Listeriaceae; Listeria.  
 OX NCBI\_TaxID=1642;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CJLP 11262 / Serovar 6a;  
 RX MEDLINE=21537279; PubMed=11679669;  
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
 RA Bagner F., Berche P., Bloecher H., Brandt P., Chakraborty T.,  
 RA Charbit A., Chetouani F., Couve E., de Darvavaz A., Dehoux P.,  
 RA Domian E., Dominguez-Bernal G., Duchaud E., Durant I., Dussurget O.,  
 RA Entian K.-D., Fihini H., Garcia-del Portillo F., Garrido P.,  
 RA Gautier L., Goebel W., Gomez-Lopez M., Hain T., Hauf J., Jackson D.,  
 RA Jones L.M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,  
 RA Madueno E., Maitouram A., Mata Vicente J., NG E., Nedjari H.,  
 RA Nordstroem G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,  
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tellez R.,  
 RA Vacquez-Boland J.-A., Voss H., Wheland J., Cossart P.,  
 RT "Comparative genomics of Listeria species.";  
 RL Science 294:849-852(2001).  
 DR EMBL; ALB96170; CAG97285.1; -.  
 PIR: AE1699; AE1699;  
 DR ListiList; LIN02055; -.  
 DR GO; GO:0016998; Ricciell L.; wall catabolism; IEA.  
 DR InterPro; IPR024932; IySM.  
 DR Pfam; PF01476; IySM; I.  
 DR SMART; SM00257; IySM; I.  
 KW Hypothetical protein; complete proteome.  
 SQ SEQUENCE 243 AA; 2563 MW; 62493D143B159D1 CRC64;  
 Query Match 42.3%; Score 90; DB 16; Length 243;  
 Best Local Similarity 45.5%; Pred. No. 0.18; Indels 22; Gaps 2;  
 Matches 30; Conservative 3; Mismatches 11; Indels 22; Gaps 2;  
 Qy 1 AKVVA-KKAKAKKAKKAKKAEEKA---AKYEAAYEAA 38  
 ID Q8RJ36 PRELIMINARY; PRT; 182 AA.  
 AC 08RJ36;  
 DT 01-JUN-2002 (TREMBrel. 21, Created)  
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
 DE Histone-like protein Bph2 (Fragment).  
 GN BPH2.  
 OS Burkholderia multivorans.  
 OC Bacteriia; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia.  
 OX NCBI\_TaxID=87883;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Khotti A., Plesa M., Cornelis P.;  
 RA RT "Mini-Tropri, a new mini-transposon for in vivo protein epitope  
 RT tagging.", (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RL Submitted; AY089703; AACN09090\_2; -.  
 DR NON\_TER 182 182  
 FT SEQUENCE 182 AA; 18768 MW; 243C5AECDASA0234 CRC64;  
 Query Match 41.8%; Score 89; DB 2; Length 182;  
 Best Local Similarity 50.4%; Pred. No. 0.18; Indels 6; Gaps 3;  
 Matches 29; Conservative 3; Mismatches 10; Indels 6; Gaps 3;  
 Qy 1 AKVVA-KKAKAKKAKKAKKAEEKA 42  
 ID Q88N16 PRELIMINARY; PRT; 372 AA.  
 AC 088N16;  
 DT 01-JUN-2003 (TREMBrel. 24, Created)  
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBrel. 25, Last annotation update)  
 DE Biopolymer transport protein Tola.

RESULT 14  
 ID Q9WWX1 PRELIMINARY; PRT; 372 AA.  
 AC Q9WWX1;  
 DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 DE Tola protein.  
 RN GN Pseudomonas putida.  
 RC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mt-2;  
 RX MEDLINE=96198174; PubMed=6626299;  
 RA Rodriguez-Hervia J.J., Ramos-Gonzalez M.I., Ramos J.;  
 RT "The Pseudomonas putida peptidoglycan-associated outer membrane  
 lipoprotein (PAL) is involved in maintenance of the integrity of the  
 cell envelope";  
 RL J. Bacteriol. 178:1699-1706(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mt-2;  
 RA Ramos-Gonzalez M.I.;  
 RL Submitted (JUN 1995) to the EMBL/GenBank/DDJB databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mt-2;  
 RA Rodriguez-Hervia J.J.;  
 RL Submitted (JUL 1999) to the EMBL/GenBank/DDJB databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mt-2;  
 RX MEDLINE=96420022; PubMed=8824639;  
 RA Rodriguez-Hervia J.J., Ramos J.;  
 RT "Characterization of an Oprl null mutant of Pseudomonas putida.";  
 RL J. Bacteriol. 178:5836-5840(1996).  
 DR EMBL; X74218; CAB50780\_1; -.  
 DR GO; GO:0000786; C:nucleosome; IEA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:003677; F:DNA binding; IEA.  
 DR GO; GO:0003334; P:nucleosome assembly; IEA.  
 DR InterPro; IPR005819; Histone\_H5.  
 DR Prints; PR00624; HistonH5.  
 DR TIGR01352; tomb\_Cterm; 1.  
 DR SEQUENCE 372 AA; 40133 MW; 87F49795ECC3C0BC CRC64;  
 Query Match 41.5%; Score 88.5; DB 2; Length 372;  
 Best Local Similarity 39.7%; Pred. No. 0.39; Indels 23; Gaps 1;  
 Matches 27; Conservative 8; Mismatches 10; Indels 23; Gaps 1;

Qy 1 AKVVA-KKAKAKKAKKAKKAEEKA 37  
 ID Q88N16 PRELIMINARY; PRT; 372 AA.  
 AC 088N16;  
 DT 01-JUN-2003 (TREMBrel. 24, Created)  
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

GN TOLIA OR PP1221.  
 OS Pseudomonas putida (strain KT2440).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID:160488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22423060; PubMed=12534463;  
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
 RA Martin dos Santos V.A.P., Fouls D.E., Gill S.R., Pop M., Holmes M.,  
 RA Brinkac L., Bearan M., Detter C., Daugherty S., Kolonay J.,  
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,  
 RA Chris Lee P., Holtzapfel B., Scanlan D., Iran K., Moazzez A.,  
 RA Utterback T., Rizzo M., Lee K., Konack D., Moestl D., Wedler H.,  
 RA Lauwer J., Stjepanic D., Hoheisel J., Straetz M., Heim S.,  
 RA Kiewitz C., Eisen J., Timmis K.N., Dueberhoef A., Tuemmler B.,  
 RA Fraser C.M.,  
 RT "complete genome sequence and comparative analysis of the  
 metabolic versatility of Pseudomonas putida KT2440";  
 RL Environ. Microbiol. 4:799-808(2002).  
 DR EMBL; AB016778; ANN66845.1; -.  
 DR TIGR; PP1221; -.  
 DR GO; GO:0000786; C:nucleosome; IEA.  
 DR GO; GO:005334; C:nucleus; IEA.  
 DR GO; GO:03677; F:DNA binding; IEA.  
 DR GO; GO:006334; P:nucleosome assembly; IEA.  
 DR InterPro; IPR001819; Histone\_H5.  
 DR PRINTS; PRO0624; HISTONEH5.  
 KW Complete proteome.  
 SQ SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;  
 Query Match 41.5%; Score 88.5; DB 16; Length 372;  
 Best Local Similarity 39.7%; Pred. No. 0.39;  
 Matches 27; Conservative 8; Mismatches 10; Indels 23; Gaps 1;  
 QY 1 AKKTAKKAKAAKKAKAAKKAKAKTEKA-----AEKAA 37  
 DB 121 AEDEAKKAAEAKKAEEAKKAEEAKKADAKKAQDIAKKADEAKKKEEAKKA 180  
 QY 38 AKKAAVEA 45  
 DB 181 AEAKKKA 188

Search completed: April 20, 2004, 23:17:44  
 Job time : 23.039 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 23:08:29 ; Search time 29.2208 seconds  
(without alignments) 435.123 Million cell updates/sec

Title: US-09-816-989a-2

Perfect score: 213

Sequence: 1 ARKKAKAKAKAKAKAKAKA..... AKYEKAEEKAEEAYEA 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: geneseq\_23jan01;\*
- 2: geneseq1980;\*
- 3: geneseq2000s;\*
- 4: geneseq2001s;\*
- 5: geneseq2002s;\*
- 6: geneseq2003s;\*
- 7: geneseq2004s;\*
- 8: geneseq2004s;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	213	100.0	AAY82572	AY82572 Copolymer
2	138	64.8	AAY82577	AY82577 Copolymer
3	134.5	63.1	AAY82573	AY82573 Copolymer
4	131	61.5	AAY82575	AY82575 Copolymer
5	126.5	59.4	AAY82576	AY82576 Copolymer
6	120.5	56.6	AAY82574	AY82574 Copolymer
7	108.5	50.9	AAY82724	AY82724 Protein e
8	103	50.7	AAY82571	AY82571 Copolymer
9	99.5	46.7	AAR0446	Aar06446 Recombina
10	93	45.0	AAR28871	Aar28871 High affi
11	90	46.0	ABU28559	Abu28559 Protein e
12	95	44.6	ABU31397	Abu31397 Protein e
13	94.5	44.4	ABB49123	Abb49123 Listeria
14	94	44.4	ABU32619	Abu32619 Protein e
15	94	44.1	AAR0445	Aar06445 Recombina
16	91	42.7	ABAY4928	Aay14928 Amino aci
17	91	42.7	ABP70903	Abp70903 Mycobacte
18	89.5	42.0	ABY34055	Aby34055 M. tuberc
19	89.5	42.0	ABY5353	Aby5353 M. tuberc
20	89.5	42.0	ABU4623	Abu34623 Protein e
21	89.5	42.0	ABU38893	Abu36893 Protein e
22	87.5	41.5	ABU40185	Abu40185 Protein e
23	87	40.8	ABG28693	Abg28693 Novel hum
24	86	40.4	ABW44934	Aaw44934 Mycobacte
25	86	40.4	RAW43082	Aaw43082 Mycobacte

**ALIGNMENTS**

Result No.	Score	Query Match Length	DB ID	Description
1	213	100.0	AAY82572	AY82572 standard; peptide; 45 AA.
2	138	64.8	AAY82577	AY82577;
3	134.5	63.1	AAY82573	AY82573;
4	131	61.5	AAY82575	AY82575;
5	126.5	59.4	AAY82576	AY82576;
6	120.5	56.6	AAY82574	AY82574;
7	108.5	50.9	AAY82724	AY82724;
8	103	50.7	AAY82571	AY82571;
9	99.5	46.7	AAR0446	06-APR-2000.
10	93	45.0	AAR28871	24-SEP-1999;
11	90	46.0	ABU28559	99WO-US022402.
12	95	44.6	ABU31397	25-SEP-1998;
13	94.5	44.4	ABB49123	98US-0101693P.
14	94	44.4	ABU32619	(YEDA ) YEDA RES & DEV CO LTD.
15	94	44.1	AAR0445	PA (TEVA) TEVA PHARM USA INC.
16	91	42.7	ABAY4928	PI Gad A, Lis D;
17	91	42.7	ABP70903	XX
18	89.5	42.0	ABY34055	WPI; 2000-317499/27.
19	89.5	42.0	ABY5353	PT: 2000-317499/27.
20	89.5	42.0	ABU4623	Copolymer 1 related polypeptides used as molecular weight markers for
21	89.5	42.0	ABU38893	glutamine acetate and for treatment and prevention of immune diseases.
22	87.5	41.5	ABU40185	XX
23	87	40.8	ABG28693	XX
24	86	40.4	ABW44934	XX
25	86	40.4	RAW43082	XX

CC weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

Sequence 45 AA:

Query Match	100.0%	Score	213	DB	3	Length	45
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	45	; Conservative		0		Mismatches	0
ID	AY82577	standard; peptide;	109	AA.		Indels	0
AC	AY82577;					Gaps	0

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

RESULT 2

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	100.0%	Pred.	No.	2	4e-16		
Matches	1	AKEYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
ID	AY82577	standard; peptide;	109	AA.			
XX							

weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

Sequence 109 AA:

Query Match	64.8%	Score	138	DB	3	length	109
Best Local Similarity	76.6%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKA--KKEYAAEAKKAKAYKAEEAKKA	109	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

RESULT 3

Query	1	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45				
Best Local Similarity	64.8%	Pred.	No.	8	8e-08		
Matches	36	; Conservative		0		Mismatches	7
ID	65	AKKYAKAKAEGAKKAYKAEEAKKAKEKAKAAYEA	45	AA		Indels	4
AC	AY82573	standard; peptide;	56	AA.		Gaps	2
XX							

XX  
PS Claim 10; Page 14; 72pp; English.

XX  
XX  
CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polyptides from the present invention. The present invention describes polyptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polyptides of the invention are used as molecular weight markers for glatiramer acetate related terrapolymers. The polyptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polyptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

XX SQ Sequence 56 AA;

Query Match 63.1%; Score 134.5; DB 3; Length 56;  
Matches 39; Conservative 0; Mismatches 5; Indels 13; Gaps 4;

QY 1 AKKYAKK---AKA-EKA---K-KAY-KAA-EKK-A-KAA-KAA-KAY-EA 45  
Db 1 AKK-YAKKEK-KYAK-KGKE-KAA-KAA-KAY-KAA-EKK-KAA-EAK-Y-K-K-EA 56

RESULT 4  
AAY82575  
ID AAY82575 standard; peptide; 77 AA.

XX AAY82575;  
AC  
XX DT 28-JUL-2000 (first entry)

DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.  
XX  
KW Copolymer; molecular weight marker; TV-marker; immune disease;  
KW glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;  
KW osteoprotic; immunosuppressive; antithyroid; antiinflammatory;  
KW antidiabetic; thiomimetic; hematologic; antiparotic; dermatological;  
KW antiinfective; immunosuppressive; demyelinating disease; osteoarthritis;  
KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;  
KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;  
KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;  
KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;  
OS Unidentified.  
PN WO20018794-A1.

XX PD 06-APR-2000.  
PP 24-SEP-1999; 99WO-US022402.  
XX PR 25-SEP-1998; 98US0-0101693P.  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA (TEVA-) TEVA PHARM USA INC.  
XX PI Gad A, 11B D;

DR WPI; 2000-317499/27.

XX PT Copolymer 1 related polyptides used as molecular weight markers for

XX PT glatiramer acetate and for treatment and prevention of immune diseases.

CC CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polyptides from the present invention. The present invention describes polyptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polyptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polyptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polyptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

XX SQ Sequence 77 AA;

Query Match 61.5%; Score 131; DB 3; Length 77;  
Matches 39; Conservative 0; Mismatches 6; Indels 32; Gaps 3;

QY 1 AKKYAKK---AKA-EKA---K-KAY-KAA-EKK-A-KAA-KAY-EA 29  
Db 1 AKKYAKK-EK-KYAK-KGKE-KAA-KAA-KAY-KAA-EKK-KAA-EAK-Y-K-K-EA 60

QY 30 -KAA-KAA-KAY-EA 45  
Db 61 YK-EAA-KAA-KAY-EA 77

RESULT 5  
AAY82576  
ID AAY82576 standard; peptide; 86 AA.

XX AC AAY82576;  
XX DT 28-JUL-2000 (first entry)

DE Copolymer Molecular weight TV-marker amino acid sequence SEQ ID NO:6.  
XX  
KW Copolymer; molecular weight marker; TV-marker; immune disease;  
KW glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;  
KW osteoprotic; immunosuppressive; antithyroid; antiinflammatory;  
KW antidiabetic; thiomimetic; haemostatic; antipsoriatic; dermatological;  
KW antiinfective; immunosuppressive; demyelinating disease; osteoarthritis;  
KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;  
KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;  
KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;  
KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;  
KW pemphigus vulgaris; systemic lupus erythematosus.  
OS Unidentified.

XX PN WO20018794-A1.  
XX PD 06-APR-2000.  
PP 24-SEP-1999; 99WO-US022402.  
XX PR 25-SEP-1998; 98US0-0101693P.  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA (TEVA-) TEVA PHARM USA INC.  
XX PI Gad A, 11B D;

DR WPI; 2000-317499/27.

XX PT Copolymer 1 related polyptides used as molecular weight markers for

XX PT glatiramer acetate and for treatment and prevention of immune diseases.

CC CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polyptides from the present invention. The present invention describes polyptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polyptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polyptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polyptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

PR 25-SEP-1998; 98US-0101693P.  
 XX PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (TEVA-) TEVA PHARM USA INC.  
 XX PI Gad A, Lis D;  
 XX DR WPI; 2000-317499/27.  
 PT Copolymer 1 related polypeptides used as molecular weight markers for  
 glatiramer acetate and for treatment and prevention of immune diseases.  
 XX PS Claim 10; Page 14; 72pp; English.  
 CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular  
 weight TV-marker polypeptides from the present invention. The present  
 invention describes Polypeptides {1} for determining the molecular weight  
 of a copolymer (CP), which has an identified molecular weight and an  
 amino acid composition corresponding to the copolymer. The polypeptides  
 of the invention are used as molecular weight markers for glatiramer  
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 treating and preventing immune diseases in a mammal. Autoimmune diseases  
 which may be treated include either cell-mediated or antibody-mediated  
 diseases. Such diseases include arthritic conditions, demyelinating  
 arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune  
 cophritis, autoimmune thyroiditis, autoimmune ureteritis, Crohn's  
 disease, chronic immune thrombocytopenia purpura, colitis, contact  
 sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barré's  
 syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,  
 psoriasis, pityriasis vulgaris, or systemic lupus erythematosus. Mediated-  
 mediated diseases which can be treated include host-versus-graft disease,  
 graft-versus-host disease, and delayed-type hypersensitivity. The  
 properties of the invention have defined molecular weights and physical  
 properties which are analogous to glatiramer acetate molecules, which  
 makes them ideal for use as molecular weight markers  
 XX SQ Sequence 86 AA;

Query	Match	Score	DB	Length
AAY82574	Best Local Similarity	59.4%	3	86;
ID AAY82574	Matches	45.3%	Pred. No.	1.2e-06;
XX AC AAY82574;	Matches	39;	Mismatches	0;
XX DT 28-JUL-2000 (first entry)	Conservative	0;	Indels	41;
XX DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.	Gaps	3		
KW Copolymer; molecular weight marker; TV-marker; immune disease;	QY 1 AKKCYAKK-----AKAEKA-----KKYKAAKKCKAYE-----	29		
KW glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;	Db 1 AKKTYAKKEKAYAKKAEEKAKEAKYAKKAEEAKKAKAEEKEYAAEAK	60		
KW osteoprotective; immunosuppressive; antithyroid; antinflammatory;	QY 30 -----KAEEKAKEAYEA 45			
KW anti-diabetic; triyromimetic; haemostatic; anti-psoriatic; dermatological;	Db 61 YKREAAKKAKAYKAEEAKAEEAYEA 86			

RESULT 6

OS Unidentified.  
 PN WO200018794-A1.  
 XX  
 PD XX  
 XX 05-APR-2000.  
 PF XX  
 PR 24-SEP-1999; 99WO-US022402.  
 XX 25-SEP-1998; 98US-0101693P.  
 XX  
 PA (TEVA) YEDA RES & DEV CO LTD.  
 PA (TEVA-) TEVA PHARM USA INC.  
 PT XX  
 PI Gad A, Lib D;  
 DR XX  
 PT XX  
 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.  
 PS XX  
 Claim 10; Page 14; 72pp; English.  
 XX  
 AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight IV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or Systemic lupus erythematosus. Mediated-diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers.  
 XX  
 Sequence 66 AA;  
 SQ  
 Query Match 56.6%; Score 120.5; DB 3; Length 66;  
 Best Local Similarity 71.1%; Pred. No. 4.2e-06;  
 Matches 32; Conservative 0; Mismatches 6; Indels 7; Gaps 2;  
 QY  
 1 AKKYAKAKAKAKYAKKAKYAAEAKKAKAYAAEAKKAKAYAA 45  
 Db 29 AKKYAKAKAKAE-KKYAAEAK--YKAEEAKAAYEA 66  
 result 7  
 ABU27824  
 ID ABU27824 standard; protein; 428 AA;  
 AC XX  
 AC ABU27824;  
 DT XX  
 19-JUN-2003 (first entry)  
 DE Protein encoded by Prokaryotic essential gene #13351.  
 KW XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 OS OS  
 XX Enterobacter cloacae.  
 PN WO200277183-A2.

PD 03-OCT-2002.

XX XX

PF 21-MAR-2002; 2002WO-US009107.

XX XX

PR 21-MAR-2001; 2001US-00815242.

KW 06-SEP-2001; 2001US-0048893.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX XX

PA (ELTR-) ELUTRA PHARM INC.

XX XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlben KL, Zyskind JW;

PI Wall D, Trawick JP, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;

XX XX

WPI; 2003-02926/02.

OS DR N-PSDB; ACR31594.

XX XX

PT New antisense nucleic acids, useful for identifying proteins or screening PT for homologous nucleic acids required for cellular proliferation to PT isolate candidate molecules for rational drug discovery programs.

PS XX

Claim 25; SEQ ID NO 55748; 1766pp; English.

XX XX

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 428 AA;

XX XX

Query Match 50.9%; Score 108; 5; DB 6; Length 428;

Matches 32; Conservative 2; Mismatches 8; Indels 11; Gaps 2;

SQ Sequence 35 AA;

XX XX

Query Match 50.7%; Score 108; DB 3; Length 35;

Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

SQ Sequence 35 AA;

XX XX

Query Match 50.4%; Score 108; DB 3; Length 35;

Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

SQ Sequence 35 AA;

XX XX

Query Match 50.4%; Score 108; DB 3; Length 35;

Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

SQ Sequence 35 AA;

XX XX

Query Match 50.4%; Score 108; DB 3; Length 35;

Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

SQ Sequence 35 AA;

XX XX

Query Match 50.4%; Score 108; DB 3; Length 35;

Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

SQ Sequence 35 AA;

XX XX

Query Match 50.4%; Score 108; DB 3; Length 35;

Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

SQ Sequence 35 AA;

XX XX

d† 28-JUL-2000 (first entry)

XX DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.

XX KW Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteoarthritic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antisporotic; dermatological; antiamebic; immunosuppressive; demyelinating disease; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopenia; psoriasis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; Hashimoto's disease; idiopathic myxoeedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

XX KW Unidentified.

XX PN WO20018794-A1.

XX PD 06-APR-2000.

XX PR 24-SEP-1999; 99WO-US022402.

XX PI Gad A, Lis D; DR XX

XX WPI; 2000-317499/27.

XX PS Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

XX Claim 10; Page 14; 72pp; English.

XX AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoeedema, myasthenia gravis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers.

XX Sequence 35 AA;

XX Query Match 50.7%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

XX Query Match 50.4%; Score 108; DB 3; Length 35;

XX Matches 29; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

XX SQ Sequence 35 AA;

ID AAR06446 standard; protein; 105 AA.  
 XX  
 AC AAR06446;  
 XX 03-JAN-1991 {revised}  
 DT Recombinant copolymer 1-19, myelin basic protein analogue.  
 KW Recombinant copolymer 1; COP-1-19; myelin basic protein; MEF; multiple sclerosis.  
 KW immunological activity; autoimmune encephalomyelitis; multiple sclerosis.  
 KW Synthetic.  
 XX OS Synthetic.  
 XX  
 PN BP383620-A.  
 XX  
 PD 22-AUG-1990.  
 XX  
 PT 16-FEB-1990; 90EP-00301700.  
 XX  
 PR 17-FEB-1989; 89US-00312541.  
 PR 07-FEB-1990; 90US-00473845.  
 XX  
 PA (REPK ) REPLIGEN CORP.  
 XX  
 PI Cook KS;  
 DR WPI; 1990-255848/34.  
 XX  
 PT producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.  
 XX Disclosure; Fig 12; 25pp; English.  
 PS  
 XX  
 CC To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-Nov-1984 US469109, NRRRL B-15910) a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, protein A, and rCOP-1 sequences. A methionine residue occurs between the protein A and rCOP-1 sequences originating from the 5'-linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes encoding the following segments: YKK, AEE, RAK, ERA, KKA, YEA, AKA, KKA, and AAA. The N-terminal alanine residue is left behind following C-terminal cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g., multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids. See also AAQ05664. (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 CC  
 CC SQ Sequence 106 AA:  
 Best Local Similarity 46.7%; Score 99.5; DB 2; Length 106;  
 Matches 58.3%; Pred. No. 0.0013; Mismatches 4; Indels 9; Gaps 2;  
 OY 3 KYAKKA-KAEKAKKAKYAKKAELKAKEAKKAA-----AKEA 41  
 Db 8 KAAKKAYEAKKAKYAKKAELKAKEAKKAAKEAKKAKEAKKA 55  
 RESULT 10  
 AAR2881 AAR2881 standard; peptide; 46 AA.  
 XX  
 AC AAR2881;  
 XX 25-MAR-2003 (revised)  
 DT 23-MAR-1993 (first entry)  
 XX  
 DE High affinity macrophage mannose receptor ligand compound #9.  
 DX  
 KW glycopptide; mannose; mannosylated; glycosylated; mannose receptor;  
 KW macrophages; monocytes; destroy; cytotoxicity; label; image; alter;  
 KW inflammatory diseases; macrophage secretory products; Crohn's disease;  
 KW legionnaires disease; mononuclear phagocytes; HIV; AIDS;  
 KW lysosomal storage diseases; Gaucher's disease; asthma;  
 KW alveolar macrophages metastasis; systemic macrophages; deliver;  
 KW antigenic peptides; prevent transplant rejection; organ transplantation;  
 KW antitumour agents; cancer; toxins.  
 XX OS Synthetic.  
 XX  
 FH Key  
 PT Modified-site 1  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine. May also have non interfering substs."  
 PT Modified-site 4  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 7  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 10  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 13  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 16  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 19  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 22  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 25  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 28  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 31  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 34  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 37  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine."  
 PT Modified-site 40  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
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 PT Modified-site 43  
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 PT Glucosamine."  
 PT Modified-site 46  
 PT /note= "opt may have mannose, fucose, glucose or N-AC-  
 PT Glucosamine. May also have non interfering substs."  
 XX  
 PN WO9219248-A1.  
 XX  
 DD 12-NOV-1992.  
 XX  
 PR 01-MAY-1992; 92WO-US003609.  
 XX  
 PR 03-MAY-1991; 91US-00694983.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.



PR	25-OCT-2001; 2001US-0342223P.	XX	Listeria monocytogenes.
PR	08-FEB-2002; 2002US-0007851.	OS	
PR	06-MAR-2002; 2002US-036299P.	XX	
XX		PN	WO200177335-A2.
PA	(ELIT- ) ELITRA PHARM INC.	XX	
PT	Wang L, Zamudio C, Malone C, Haselbeck R, Olsen KU, Zyskind JW;	XX	
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	XX	
XX		XX	
DR	WPI; 2003-229926/02.	XX	
DR	N-PSTD; ACA35267.	XX	
PT	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.	XX	
PT	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:	XX	
CC	(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> , <i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences	XX	
XX	XX	XX	
SQ	Sequence 323 AA;	XX	
Query Match	44.5%; Score 95; DB 6; Length 323;	XX	
Best Local Similarity	52.9%; Pred. No. 0.013;	XX	
Matches	27; Conservative 4; Mismatches 14; Indels 6; Gaps 1;	XX	
QY	1 AKKYAKKAKEAKKAKYKAERK-----KAKYKEKAKEKAAYEA 45	XX	
Db	92 AAEQKQKAEEAAKQOQEAEKAOKAEEKAEEKAEEKAQKAQKA 142	XX	
RESULT 13		XX	
ABB49123	ABB49123 standard; protein; 239 AA.	XX	
XX		XX	
AC	ABB49123;	XX	
DT	05-FEB-2002 (first entry)	XX	
DE	Listeria monocytogenes protein #1827.	XX	
XX		XX	
KW	Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; Vitamin B12; bacterial infection; disease.	XX	
OS	Listeria monocytogenes.	XX	
XX		XX	
PA	18-OCT-2001.	XX	
PT	Buchrieser C, Frangeul L, Couve E, Rusniok C, Fathi H, Detour P;	XX	
PI	Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunert F, Cosset P;	XX	
PI	Daniel J, Goebel W, Kraft J, Kuhn M, Ng E, Vaquez-Boland JA;	XX	
PI	Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez R, Amend A;	XX	
PI	Chakraborty T, Domain E, Hain T, Berche P, Charbit A, Duran L;	XX	
PI	Perez-Diaz J, Baguerco F, Garcia del Portillo F, Gomez-Lopez N;	XX	
PI	Madueno E, De Pablo B, Weiland J, Kaerst U, Entian K, Hauf J;	XX	
PI	Rose M, Voss H;	XX	
DR	WPI; 2002-010914/01.	XX	
PS	Genomic sequence for <i>Listeria monocytogenes</i> ; useful e.g. for treatment and prevention of <i>Listeria</i> and related bacterial infections, and related polypeptides.	XX	
XX		XX	
SQ	Claim 6; SEQ ID NO 1828; 192pp; French.	XX	
XX		XX	
CC	The present invention relates to the genome sequence of <i>Listeria monocytogenes</i> EGD-e (see ABA0341). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in <i>L. monocytogenes</i> and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of <i>L. monocytogenes</i> and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate <i>L. monocytogenes</i> related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by <i>L. monocytogenes</i> and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences	XX	
XX		XX	
SQ	Sequence 239 AA;	XX	
Query Match	44.4%; Score 94.5; DB 5; Length 239;	XX	
Best Local Similarity	56.2%; Pred. No. 0.011;	XX	
Matches	27; Conservative 7; Mismatches 9; Indels 5; Gaps 2;	XX	
QY	2 KKYAKKAKEAKKAKYKAERK--AKYKEKAEEKAEEKAAYEA 44	XX	
Db	124 KAAEKAEDKICKQEEDAVKANKKQEEAKAEEKAEEKAQKA 171	XX	
RESULT 14		XX	
ABU32619	ABU32619 standard; protein; 239 AA.	XX	
ID		XX	
AC	ABU32619;	XX	
XX		XX	
DT	19-JUN-2003 (first entry)	XX	
XX		XX	
DE	Protein encoded by Prokaryotic essential gene #18146.	XX	
XX		XX	
KW	Antisense; Prokaryotic essential gene; cell proliferation; drug design.	XX	
OS	Listeria monocytogenes.	XX	

Page 6

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: April 20, 2004, 23:17:50 ; Search time 22.2078 seconds

(without alignments) 58.601 Million cell updates/sec

Title: US-09-816-989a-2

Perfect score: 213 AKKYAKKAKAKAKAKYKAA..... AKYEKAEEKAEEAYEA 45

Sequence:

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEM\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

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17: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Match Length	DB ID	Description
1	213	100.0	45	Sequence 2, Appli
2	138	64.8	109	Sequence 7, Appli
3	134.5	63.1	56	Sequence 3, Appli
4	131	61.5	9	Sequence 4, Appli
5	126.5	59.4	86	Sequence 5, Appli
6	120.5	56.6	9	Sequence 6, Appli
7	108.5	50.9	428	Sequence 45, Conserv
8	9	50.7	12	Sequence 4, Appli
9	98	46.0	421	Sequence 1, Appli
10	95	44.6	323	Sequence 1, Appli
11	94.5	44.4	12	Sequence 1, Appli
12	91	42.7	223	Sequence 1, Appli
13	91	42.7	223	Sequence 1, Appli
14	89.5	42.0	214	Sequence 1, Appli
15	89.5	42.0	214	Sequence 1, Appli

**ALIGNMENTS**

RESULT 1  
US-09-816-989a-2  
Sequence 2, Application US/09816989A  
; Patent No. US20020115103A1  
; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; ATTORNEY: Lis, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKER  
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE  
; FILE REFERENCE: 2609/60807-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09816, 899A  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/101, 693  
; PRIOR FILING DATE: 1998-01-25  
; PRIOR APPLICATION NUMBER: PCT/US99/22402  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
; US-09-816-989a-2  
Query Match Similarity 100.0%; Score 213; DB 9; Length 45;  
Best Local Similarity 100.0%; Score 213; DB 9; Length 45;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Sequence 1, Appli  
QY  
1 AKKYAKKAKAKAKAKYKAAEKAKAKYKAAEKAKERATEA 45  
|||||||  
Sequence 56483, A  
Sequence 59321, A  
Sequence 60543, A  
Sequence 2011, A  
Sequence 52, A  
Sequence 62547, A  
Sequence 64817, A  
; Sequence 7, Application US/09816989A



US-09-816-989A-4  
; Sequence 4, Application US/09816989A  
; Patent No. US20030115103A1  
; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK  
; FILE REFERENCE: 2609/60807-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/816,989A  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/101,693  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: PCT/US99/22402  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 4  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-4  
Query Match 56.6%; Score 120.5; DB 9; length 66;  
Best local Similarity 71.1%; Pred. No. 3.1e-06; Mismatches 6; Indels 7; Gaps 2;  
Matches 32; Conservative 0; Mismatches 6; Indels 7; Gaps 2;  
Qy 1 AKKYAKKAKKEKAKGAKYKAEEAKGAKAKAAKEAYEA 45  
Db 29 AKKYAKKAKKEKAKGAKYKAEEAKGAKAKAAKEAYEA 66  
RESULT 7  
US-10-282-122A-55748  
Sequence 55748, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Olsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Travick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,948  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2001-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09

RESULT 8  
US-09-816-989A-1  
; Sequence 1, Application US/09816989A  
; Patent No. US20030115103A1  
; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; APPLICANT: Lis, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK  
; FILE REFERENCE: 2609/60807-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/816,989A  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/101,693  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: PCT/US99/22402  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 1  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-1  
Query Match 50.9%; Score 108.5; DB 12; length 428;  
Best local Similarity 60.4%; Pred. No. 0.00047; Mismatches 2; Indels 11; Gaps 2;  
Matches 32; Conservative 2; Mismatches 8; Indels 11; Gaps 2;  
Qy 1 AKKAANDAQKGEAEAKKQAEEKKAAEAKGAAEKAEEKA 42  
Db 199 AKKAANDAQKGEAEAKKQAEEKKAAEAKGAAEKAEEKA 251  
RESULT 9  
US-10-282-122A-56493  
Sequence 56493, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Olsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Travick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA\_034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/205,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 56483  
 LENGTH: 421  
 TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 US-10-282-122A-56483  
 Query Match 46.0%; Score 98; DB 12; Length 421;  
 Best Local Similarity 65.3%; Pred. No. 0.0054; Mismatches 9; Indels 6; Gaps 3;  
 Matches 32; Conservative 2;  
 APPLICANT: Wang, Liangbu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forseyh, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA\_034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/205,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 59321  
 LENGTH: 323  
 TYPE: PRT  
 ; ORGANISM: Klebsiella pneumoniae  
 US-10-282-122A-59321  
 Query Match 44.6%; Score 95; DB 12; Length 323;  
 Best Local Similarity 52.9%; Pred. No. 0.01; Mismatches 4; Indels 6; Gaps 1;  
 Matches 27; Conservative 4;  
 APPLICANT: Wang, Liangbu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forseyh, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA\_034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/205,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 6043  
 LENGTH: 239

TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-10-282-122A-60543

Query Match Best Local Similarity 55.2%; Pred. No. 0.0083; DB 12; length 239; Matches 27; Conservative 7; Mismatches 9; Indels 5; Gaps 2;

RESULT 12  
US-10-051-643-201  
Sequence 201, Application US/10051643  
Publication No. US20020197265A1

GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment of Immunologically-Mediated Diseases of the Respiratory System using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008C2  
CURRENT APPLICATION NUMBER: US/10/051,643  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US09/156,181

PRIOR APPLICATION NUMBER: US 08/996,624  
PRIOR FILING DATE: 1997-12-23  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 201  
LENGTH: 223  
TYPE: PRT

; ORGANISM: Mycobacterium vaccae  
US-10-051-643-201

Query Match Best Local Similarity 59.6%; Pred. No. 0.019; DB 13; length 223; Matches 28; Conservative 5; Mismatches 12; Indels 2; Gaps 2;

QY 1 AKKYAKKAKKAKKAYKAEEAKKAAYEKA-AEKAAKEAAYEA 44  
Db 124 KAAAKKAKKAKKOBEDATAKANKKKEBAAEKAADAKAAKAAKAA 171

RESULT 13  
US-10-205-979-52  
Sequence 52, Application US/10205979  
Publication No. US20030147861A1

GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Tan, Paul L. J.

APPLICANT: Abernethy, Nevin

TITLE OF INVENTION: Compounds and Methods for the Modulation of Immune Responses

FILE REFERENCE: 11000.1063U  
CURRENT APPLICATION NUMBER: US/10/205,979  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/308,446  
PRIOR FILING DATE: 2001-07-26  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 52  
LENGTH: 223  
TYPE: PRT

; ORGANISM: Mycobacterium vaccae  
US-10-205-979-52

Query Match Best Local Similarity 59.6%; Pred. No. 0.019; DB 14; length 223; Matches 28; Conservative 5; Mismatches 12; Indels 2; Gaps 2;

QY 1 AKKYAKKAKKAKKAKKAYKAEEAKKAAYEKA-AEKAAKEAAYEA 45  
Db 111 AKKVAKKAKKAKKATKAKKATKAPA--RKAATKAPAKKAATKA 152

RESULT 14  
US-10-282-122A-62547  
Sequence 62547, Application US/10282122A  
Publication No. US20040029129A1

GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zykind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITA.03A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/1206,849  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/1207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/1230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/1230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/1242,519  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/1253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/1257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/1267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/1269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 62547  
LENGTH: 214  
TYPE: PRT

; ORGANISM: Mycobacterium bovis  
US-10-282-122A-62547

Query Match Best Local Similarity 55.6%; Pred. No. 0.026; DB 12; length 214; Matches 25; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

QY 1 AKKYAKKAKKAKKAKKAYKAEEAKKAAYEKA-AEKAAKEAAYEA 45  
Db 111 AKKVAKKAKKAKKATKAKKATKAPA--RKAATKAPAKKAATKA 152

RESULT 15  
US-10-282-122A-64817  
Sequence 64817, Application US/10282122A  
Publication No. US20040029129A1

GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Karl  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELTRA\_034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIORITY APPLICATION NUMBER: 60/191,078  
 PRIORITY FILING DATE: 2000-03-21  
 PRIORITY APPLICATION NUMBER: 60/206,848  
 PRIORITY FILING DATE: 2000-05-23  
 PRIORITY APPLICATION NUMBER: 60/207,727  
 PRIORITY FILING DATE: 2000-05-26  
 PRIORITY APPLICATION NUMBER: 60/230,335  
 PRIORITY FILING DATE: 2000-09-06  
 PRIORITY APPLICATION NUMBER: 60/230,347  
 PRIORITY FILING DATE: 2000-09-09  
 PRIORITY APPLICATION NUMBER: 60/242,578  
 PRIORITY FILING DATE: 2000-10-23  
 PRIORITY APPLICATION NUMBER: 60/253,625  
 PRIORITY FILING DATE: 2000-11-27  
 PRIORITY APPLICATION NUMBER: 60/257,931  
 PRIORITY FILING DATE: 2000-12-22  
 PRIORITY APPLICATION NUMBER: 60/267,636  
 PRIORITY FILING DATE: 2001-02-09  
 PRIORITY APPLICATION NUMBER: 60/269,308  
 PRIORITY FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 64817  
 LENGTH: 214  
 TYPE: PRT  
 ORGANISM: Mycobacterium tuberculosis  
 US-10-282-122A-64817

Query Match 42.0%; Score 89.5; DB 12; Length 214;  
 Best Local Similarity 55.6%; Pred. No. 0.026; Gaps 1;  
 Matches 25; Conservative 4; Mismatches 13; Indels 3;  
 Qy 1 AKKYAKAKAEGAKKAYAKAAKKAKEYAKAAKAAEAYEA 45  
 Db 111 AKKVAKKAPAKKATKAAGCAATKAPA---RKATKAPAKKATKA 152

Search completed: April 20, 2004, 23:27:17  
Job time : 23.2078 secs



membrane spanning protein Tola [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli  
C; Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C; Accession: F9725  
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Goto, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Battori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A; Reference number: A99629; MUID:21156231; PMID:11258796  
A; Accession: F9725  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-394 <HAY>  
A; Cross-references: PIDN:BA00007; PIDN:BA00023; GSPDB:GN00154  
A; Experimental source: Strain O157:H7, substrain RIMD 0509952  
C; Genetics:  
A; Gene: Ecs0774

Query Match 35.0%; Score 181.5; DB 2; Length 394;  
Best local Similarity 52.2%; Pred. No. 4.7e-05;  
Matches 60; Conservative 12; Mismatches 32; Indels 11; Gaps 5;

QY 1 AKKYAKKAE---KAYAKAKAKAKKAKAKAKAADDKA---AEEAKKAADAKKKAAEAK 55  
Db 120 AEEAKQAEKKQKOEAAAKKAADAKAKAADDKA---AEEAKKAADAKKKAAEAK 177  
QY 56 AKKEAKY-KAAKAKYAKAAKAKKEKKYYAAEAKK---AEEAKAKYAAEAKA 106  
Db 178 AAEEAQKQKEAAAAAKKKAAEAAEAAEAAEAAEAAEAAEAAEAAEAAEAA 232

RESULT 3  
G85576 membrane spanning protein Tola [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli  
C; Accession: G85576  
R; Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dirlanta, E.; Potamousis, K.; Apodaca, A.; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A; Reference number: A85480; MUID:21074935; PMID:11206551  
A; Accession: G85576  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-394 <STO>  
A; Experimental source: Strain O157:H7, substrain ED933  
C; Genetics:  
A; Gene: tola

Query Match 35.0%; Score 181.5; DB 2; Length 394;  
Best local Similarity 52.2%; Pred. No. 4.7e-05;  
Matches 60; Conservative 12; Mismatches 32; Indels 11; Gaps 5;  
QY 1 AKKYAKKAE---KAYAKAKAKAKKAKAKAADDKA---AEEAKKAADAKKKAAEAK 55  
Db 120 AEEAKQAEKKQKOEAAAKKAADAKAKAADDKA---AEEAKKAADAKKKAAEAK 177  
QY 56 AKKEAKY-KAAKAKYAKAAKAKKEKKYYAAEAKK---AEEAKAKYAAEAKA 106  
Db 178 AAEEAQKQKEAAAAAKKKAAEAAEAAEAAEAAEAAEAAEAAEAAEAAEAA 232

RESULT 5  
F83525 Tola protein PA0971 [imported] - Pseudomonas aeruginosa (strain PA01)  
C; Species: Pseudomonas aeruginosa  
C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C; Accession: F83525  
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Baker, S.; Yuan, Y.; Brody, L.I.; Coulter, S.N.; Folger, R.R.; Kas, A.; Harborg, K.; Lam, J.; Lory, S.; Olson, M.V.  
Nature 405, 959-964, 2000  
A; Residues: 1-347 <STO>  
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A; Reference number: A82950; MUID:20437337; PMID:10984043  
A; Accession: F83525  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-347 <STO>  
A; Cross-references: GB:AE004530; GB:AE004091; NID:99946865; PIDN:AAG04360.1; GSPDB:GN001  
A; Experimental source: Strain PA01  
C; Genetics:  
A; Gene: tola; PA0971

Query Match 34.5%; Score 179; DB 2; Length 347;  
Best Local Similarity 49.1%; Pred. No. 5.2e-05;  
Matches 54; Conservative 17; Mismatches 29; Indels 10; Gaps 4;  
QY 66 KKAEEAKYAKAKAKAKK---KAYAKAKYAAEAKKKAAEAKYAAEAKK 59  
Db 99 QKLEQQQVAAAKABOKKQDAEARKKAQGAOKKAQKKAQKQDAIKR 158  
QY 60 AKYAKKAKYAKAKAKKEKKYYAAEAKKAAKKAKYAAEAKKA 109  
Db 159 A-EDEKK- KAEDAKKKAAEAKKAQAAEAKKAQAAEAKKA 204

RESULT 6  
AG0592 tola protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT16)  
C; Species: Salmonella enterica subsp. enterica serovar Typhi  
A; Note: this species has also been called Salmonella typhi  
C; Date: 03-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C; Accession: AG0592  
R; Partchill, J.; Dongan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaoora, P.  
Nature 413, 848-852, 2001  
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar  
A; Reference number: AB0502; MUID:21534947; PMID:11677608  
A; Accession: AG0592  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-376 <PAR>

RESULT 4  
A25550 histone H1 - sea urchin (*Lytechinus pictus*)  
C; Species: Lytechinus pictus (painted urchin)  
C; Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 23-Jul-1999  
C; Accession: A25550  
R; Knowles, J.A.; Childs, G.J.  
Nucleic Acids Res. 14, 8121-8133, 1986  
A; Title: Comparison of the late H1 histone genes of the sea urchins *Lytechinus pictus* and







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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 20, 2004, 23:08:59 ; Search time 14.8636 Seconds  
 (without alignments)

381.848 Million cell updates/sec

Title: US-09-816-989a-7

Perfect score: 519

Sequence: I AKKYAKKAEKAYAKOKAAK..... AKAYKAEEAKAAKEAYEA 109

Scoring table: BLOSUM62  
 Gapped 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	189.5	36.5	421 TOLA_ECOLI	P19934 escherichia
2	181	34.9	210 H1_LTPT	P50600 pseudomonas
3	179	34.5	347 TOLA_PSEAB	P08695 drosophila
4	175.5	33.8	1 MSTD_DROH	P02256 parechimins
5	171.5	33.0	1391 H1_PARAN	P15869 strongyloice
6	170.5	32.9	248 H1_STRPU	Oryvgx3 drosophila
7	169.5	32.7	211 H1B_STRPU	RJ. B., Shao Y., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
8	169.5	32.7	1 MSTD_DROH	"The complete genome sequence of Escherichia coli K-12.", Science 277:1453-1474 (1997).
9	166.5	32.1	668 FAU_DROME	J. Bacteriol. 171:6600-6609 (1989).
10	165	31.8	219 H10_CHICK	[3]
11	163.5	31.5	284 TMPB_TREP	RR
12	163	31.4	224 H1L1_CHICK	SEQUENCE FROM N. A.
13	160.5	30.9	206 H1_ONCOTY	RC
14	160.5	30.9	225 H15_HUMAN	STRAIN-KL2;
15	160	30.8	208 DBH_NYCSM	MDLINE=97061202; PubMed=8905232;
16	159.5	30.7	218 H1L9_CHICK	RA
17	158	30.4	1 H14_HUMAN	Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Iton T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sampei G., Setki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horikoshi T.;
18	157	30.3	771 CALD_CHICK	RT
19	156.5	30.2	218 H1O1_CHICK	"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.", RT
20	156	30.1	885 IF2_SHEON	DNA Res. 3:137-155 (1996).
21	154.5	29.8	240 H12_VOLCA	[4]
22	153.5	29.6	372 TOLA_HAIN	DOMAINS.
23	152.5	29.4	223 H1O5_CHICK	MDLINE=91296736; PubMed=2068069;
24	151	29.1	1403 YDF3_SCHPO	RA
25	150	28.9	211 H12_MOUSE	Devergood S.K., Bevier W.F. Jr., Webster R.B.;
26	150	28.9	217 H1G_STRPU	RT
27	148	28.5	139 ASR_KLEPN	"Tola: a membrane protein involved in colicin uptake contains an extended helical region.", Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943 (1991).
28	148	28.5	217 H1_ANAPL	[5]
29	147.5	28.4	218 H14_MOUSE	INTERACTION WITH PORINS
30	147	28.3	207 H1_CAEEL	MDLINE=9713371; PubMed=8978668;
31	147	28.3	220 H13_MOUSE	Derouiche R., Gaviooli M., Benedetti H., Philipov A., Lazdunski C.,
32	146	28.1	217 H1_CHICK	P20254 salmo trutta
33	146	28.1	299 RL22_DROME	P240276 chromomus
34	144	27.7	232 H12_GLYBA	Q91761 aedes aegypt
35	144	27.7	352 ALGP_PSEAB	P40275 chironomus
36	143.5	27.6	218 H12_RAT	P18855 rattus norvegicus
37	143	27.6	214 DBH_MTCBO	P99109 mycobacterium
38	143	27.6	214 H1_NEUR	Q81012 neurospora
39	143	27.6	236 H1_CHTIE	P40277 chironomus
40	142.5	27.5	221 H1_SAINT	P02254 salmo trutta
41	142	27.4	194 H1B_CHITE	P40276 chromomus
42	141.5	27.3	232 H1B_AEDAE	Q91761 aedes aegypti
43	141.5	27.3	1 RS6_AEDAE	P40275 chironomus
44	140	27.0	232 H1A_CHITE	P02251 oryctolagus cuniculus
45	139	26.8	213 H13_RABBIT	

### ALIGNMENTS



RX MEDLINE=97113525; PubMed=8955385;  
 RA Dennis J.J., Lafontaine E.R., Sokol P.A.;  
 RT "Identification and characterization of the tolQRA genes of  
 Pseudomonas aeruginosa";  
 RL J. Bacteriol. 178:7059-7068(1996).  
 RN [2]  
 REVISIONS TO N-TERMINUS.  
 DUAN K., SOKOL P.A.;  
 Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

RP [3]  
 SEQUENCE FROM N A.  
 RP STRAIN=ATCC 15692 / PAO1;  
 RX MEDLINE=0437337; PubMed=10964043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.M.,  
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Ligrone M.,  
 Garner R.L., Goitry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 Brody L.I., Coulter S.N., Folger K.R., Kas A.B., Laribee K., Lim R.M.,  
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an  
 opportunistic pathogen." Nature 406:950-964(2000).  
 RL  
 CC -!- FUNCTION: Involved in the tonB-independent uptake of proteins (BY  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane  
 CC -!- POTENTIAL).  
 CC  
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 CC  
 CC EMBL; U30558; AAC46660.2; --.  
 DR EMBL; AED04530; AA04360.1; --.  
 DR FIR; E83525; E83525.  
 DR InterPro; IPR06260; Tomb-C.  
 DR TIGRFAMS; TIGS01352; tomb\_Cterm; 1.  
 KW Transport; Protein transport; Transmembrane; Repeat; Inner membrane;  
 KW Complete proteome.  
 FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 17 37 POTENTIAL.  
 FT DOMAIN 38 347 PERIPLASMIC (POTENTIAL).  
 FT DOMAIN 209 216 POLY-ALA.  
 SQ SEQUENCE 347 AA; 3793 MW; EEDD4B04AA095945 CRC64;  
 Query Match 34.5%; Score 179; DB 1; Length 347;  
 Matches 54; Conservative 17; Mismatches 29; Indels 10; Gaps 4;  
 CQ 6 KKAERKAYAKKAKAEEK-----KAYAKKAKAYAKKAKAEEKKAKAKKE 59  
 Db 99 QKLEQQQVAAKAKAEEKKAKAEEKAKAEEKAKAEEKKAKAKKE 158  
 CQ 60 AYKAEEKKAKAEEKKEAEEAKKAEEAKAYKAEEAKAAEAEAYEA 109  
 Db 159 A-EDEAKK-KAEDAKK-KAEDAKK-KAEEAKKAAEAKKAAEAKKAAE 204  
 RESULT 4  
 MSL1\_DROHY STANDARD; PRT; 344 AA.  
 ID MSL1\_DROHY STANDARD; PRT; 344 AA.  
 AC 008655;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Axoneme-associated protein mst101(1).  
 DE Mst101(2).  
 GN OS Drosophila hydei (Fruit fly).  
 OC Eukaryota; Metacoda; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriodea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7224;  
 RP SEQUENCE FROM N A. AND CHARACTERIZATION.  
 RX MEDLINE=95045538; PubMed=7957199;  
 RA Neeson J., Padmanabhan S., Buemann H.;  
 RT "Tandemly arranged repeats of a novel highly charged 16-amino-acid  
 motif representing the major component of the sperm-tail-specific  
 axoneme-associated protein family Dmst101 form extended  
 alpha-helical rods within the extremely elongated spermatozoa of



QY	DR	InterPro; IPR003216; Linkerhistin_N.
	DR	Pfam; PF00538; Linker histone; 1.
	DR	PRINTS; P200624; HISTONE15.
	DR	PRODOM; PDD00073; Linkerhist_N; 1.
	DR	SMART; SM00526; H15; 1.
KW	DR	Chromosomal Protein; Nuclear protein; DNA-binding; Multigene family.
SQ	SEQUENCE	211 AA; 22169 MW; 9F214581334BBB7A CRC64;
	RESULT 8	Query Match 32.7%; Score 169.5; DB 1; Length 211;
	Best Local Similarity 48.7%; Pred. No. 5.1e-05; Matches 55; Conservative 8; Mismatches 41; Indels 9; Gaps 4;	FAU_DROME STANDARD; PRT; 275 AA.
QY	3	KYAKKAA-KAYAKKA--KAAKEKKAKAKKEAKYAKAEAK-KKAKKEAKKYYAKRAK--- 55
Db	88	KLGKKRKGSDAQKAPDAKKAKLAKKEKEKKAARSKAKKEKKAKKASKTITKV 147
QY	56	-AKKEVAKYAKVAKYAKAKLEKKEVAAEKKAAKAYCAAKAAKEAA 106
Db	148	KPRAKAKKPKAKKAACKPAKPKAAKPKAKPKAAKKA 200
OS		Drosophila hydei (Fruit fly).
OC		Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.
OC		MST101(3) OR DMHST101.
GN		[11] MST3_DROHY
OS		SEQUENCE FROM N.A.
OC		MDLINE=99372678; PubMed=10445056;
OC		RA Neesen J., Heinlein U.A.O., Heinz-Glatzer K., Buennemann H.; RT "Proteins with tandemly arranged repeats of a highly charged 16-amino-acid motif encoded by the Dmht101 gene family are structural components of the outer sheath of the extremely elongated sperm tails of Drosophila hydei." Dev. Growth Differ. 41:93-99(1999).
OC		- - FUNCTION: Possible structural role in the sperm tail (By similarity).
CC		[11] TAXID=7224;
CC		SEQUENCE FROM N.A.
CC		MDLINE=20116006; PubMed=10731132;
CC		RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA George R.A., Lewis S.M., Richards S., Li P.W., Hobbs R.A., Galle R.F., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers V.-H.C., Blazej R.G., Champe M., Pfeiffer B., RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E., RA Besson K.Y., Bens P.V., Berman B.P., Bhadra D., Bolshakov S., RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandrase RA Charly J.M., Cawley S., Dahlke C., Davern P.B., Davies P., RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Durbin RA Durbin R.K., Evangelista C.C., Ferraz C., Ferriera S., Fleischman RA Fosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorreli J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum RA Kimmel B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Karpel D., Lai J.Z., RA Lasko P., Leal Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Liu X., Matteil B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milikhina N.V., Mobarry C., Morris J.C., Mosbrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Murtry D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spadring A.C., Stapleton M., Strong R., Sun E., RA Svartskas R., Tector C., Turner R., Venter E., Wang A.-H., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Wissenbach J., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Yee J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of Drosophila melanogaster." Science 287:2185-2195(2000). RL
	RESULT 9	FAU_DROME STANDARD; PRT; 668 AA.
QY	58	KAYAKAAKYYAKAKAKKEAKKAAEKK-AEAKYAKAAKAAKEAV 101
Db	107	OEAA-AOKKCAALAKKEE--AAEKKCABAARKAKKEAKERKKCEAAFK 155
DB	51	AEDVYKCKCSEAAKKKCSEAAKKEAKKEAKK---KCAEAAKKEAKKEAKKKAE
DR	997GKX3; Q95S18; O9VGXL; Q9YQ99;	FAU_DROME STANDARD; PRT; 668 AA.
AC	997GKX3; Q95S18; O9VGXL; Q9YQ99;	ID FAU_DROME STANDARD; PRT; 668 AA.
DT	28-FEB-2003 (Rel. 41; Created)	DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT	10-OCT-2003 (Rel. 42; Last annotation update)	DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE	Drosophila upregulated protein.	DE Anoxia upregulated protein.
GN	RAU or CG6554.	GN RAU or CG6554.
OS	Drosophila melanogaster (Fruit fly).	OS Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.
OX	[11] TAXID=7227;	OX NCBI_TaxID=7227;
RN	SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.
RP	STRAIN=Berkley;	RP STRAIN=canton-S; TISSUE=Head;
RC	MDLINE=99097004; PubMed=9878744;	RC MDLINE=20116006; PubMed=10731132;
RX	Ma B., Xu T., Haddad G.G.;	RX Ma B., Xu T., Haddad G.G.;
RT	"Gene regulation by O2 deprivation: an anoxia-regulated novel gene." Drosophila melanogaster." Brain Res. Mol. Brain Res. 63:217-224(1999).	RT "Gene regulation by O2 deprivation: an anoxia-regulated novel gene." Drosophila melanogaster." Brain Res. Mol. Brain Res. 63:217-224(1999).
RL	[12]	RL [12]
RP	SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC	STRAIN=Berkley;	RC STRAIN=canton-S; TISSUE=Head;
RX	MDLINE=20116006; PubMed=10731132;	RX MDLINE=99097004; PubMed=9878744;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA George R.A., Lewis S.M., Richards S., Li P.W., Hoskins R.A., Galle R.F., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers V.-H.C., Blazej R.G., Champe M., Pfeiffer B., RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E., RA Besson K.Y., Bens P.V., Berman B.P., Bhadra D., Bolshakov S., RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandrase RA Charly J.M., Cawley S., Dahlke C., Davern P.B., Davies P., RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Durbin RA Durbin R.K., Evangelista C.C., Ferraz C., Ferriera S., Fleischman RA Fosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorreli J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Karpel D., Lai J.Z., RA Lasko P., Leal Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Liu X., Matteil B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milikhina N.V., Mobarry C., Morris J.C., Mosbrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Murtry D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spadring A.C., Stapleton M., Strong R., Sun E., RA Svartskas R., Tector C., Turner R., Venter E., Wang A.-H., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Wissenbach J., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Yee J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "The genome sequence of Drosophila melanogaster." Science 287:2185-2195(2000). RL	
RN	[3]	[3]

RP REVISIONS; AND ALTERNATIVE SPLICING.

RX MEDLINE=22426059; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecny P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Wilfeld E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celtniker S.B., de Grey A.D.N.J., Drysdale R.A., Harris N.J., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S., "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review." *Genome Biol.* 3:RESEARCH0083.1-RESEARCH0083.22 (2002).

RN [4] SEQUENCE FROM N.A.

RP ISOFORM B.

RC STRAIN=Berkeley; TISSUE=Head;

RX MEDLINE=22426056; PubMed=12537569;

RA Stapleton M., Carlson J.W., Birkenstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.M., Celtniker S.E., "A *Drosophila* full-length cDNA resource.", *Genome Biol.* 3:RESEARCH0080.1-RESEARCH0080.8 (2002)

CC !- FUNCTION: Plays an important role in the regulation of tissue responsiveness to oxygen deprivation.

CC !- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=5;

CC Comment=Experimental confirmation may be lacking for some isoforms;

CC Name=A;

CC IsoId=Q9VGX3-1; Sequence=Displayed;

CC Name=B;

CC IsoId=Q9VGX3-2; Sequence=VSP\_004048, VSP\_004049;

CC Name=C;

CC IsoId=Q9VGX3-3; Sequence=VSP\_004046, VSP\_004047;

CC Name=D;

CC IsoId=Q9VGX3-4; Sequence=VSP\_004050, VSP\_004051;

CC Name=E;

CC IsoId=Q9VGX3-5; Sequence=VSP\_004052;

CC !- TISSUE SPECIFICITY: Concentrated in lamina neurons, first optic lobe neurons and cortical neurons of central brain.

CC !- INDUCTION: By anoxia.

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RESULT 10

H10\_CHICK STANDARD; PRT; 219 AA.

ID H10\_CHICK

AC P08286;

DT 01-AUG-1998 (Rel. 08, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, last annotation update)

DB Histone H1.10 (Methylated DNA binding protein-2-H1) (MDBP-2-H1).

OS Gallus gallus (Chicken).

OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87250532; PubMed=3597432;

RA Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.; Characterization of the chicken histone H1 gene complement. Generation of a complete set of vertebrate H1 protein sequences.", *J. Biol. Chem.* 262:9656-9663 (1987).

RN [2]

RP IDENTIFICATION OF ALA-13.

RX MEDLINE=9060505; PubMed=9336815;

RA Schwarz S., Hess D., Just J.P., "The methylated DNA binding protein-2-H1 (MDBP-2-H1) consists of histone H1 subtypes which are truncated at the C-terminus.", *Nucleic Acids Res.* 25:5052-5056 (1997).

CC !- FUNCTION: Histones H1 are necessary for the condensation of nucleosome chains into higher order structures.

CC !- SUBCELLULAR LOCATION: Nuclear.

CC !- SIMILARITY: Belongs to the histone H1/H5 family.

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FT RSSLSPLRIPSPVPR > RTKRPIDWIKVPPVPRPSLIS DPVTAGGRDPDERRQSLDPINRASKPDYKLAIE PYVSDTRDKNTTRDILKVRQMDTVEAGWAGRPFDSIDA OLPRURAVSESLSPYRTRYTVERNSGAMMTKSY (in Isoform B).

FT Isoform B.

FT Missing (in isoform B).

FT /FTId=VSP\_004048.

FT Missing (in isoform B).

FT /FTId=VSP\_004049.

FT Missing (in isoform D).

FT /FTId=VSP\_004051.

FT Missing (in isoform E).

FT /FTId=VSP\_004052.

FT 4507365593DD3B CRC64;

FT VARSPLIC 99 668

FT VARSPLIC 280 328

FT VARSPLIC 36 98

FT SEQUENCE 668 AA; 74487 MW; 4507365593DD3B CRC64;

FT Query Match 32.1%; Score 166 5; DB 1; Length 668;

FT Best Local Similarity 41.0%; Pred. No. 0.0002; Matches 55; Conservative 16; Mismatches 30; Indels 33; Gaps 4;

FT Matches 55; Conservative 16; Mismatches 30; Indels 33; Gaps 4;

QY 9 EKAYAKKA-KA-KKEKKYAK-YAKAYAKA-EEAKKKAKA-EAKKYAKA-K-KKEAKYAE-A 65

DB 380 EKKRAQKADEAKRREBRAEAKERDRITAEKAQAAKAAEAKIAEAEALIAEAA 439

QY 66 KKYYAKAKA-----EKKEYAALEAKKA-EAKYAKA-- 95

DB 440 QKAAEAKAKAEDAKQAEEAELAEEAQVAEEAQKAAEARIAAEAAQKAE 499

QY 96 EAAKAAKEAKAAYEA 109

DB 500 ERAQKAEEALKI 513







Om protein - protein search, using sw model Copyright (c) 1993 - 2004 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	202	38.9	395	2	Q937K4		Q937K4 erwinia chr
2	190	36.7	372	2	Q9WYX1		Q9WYX1 pseudomonas

Q8t5c8 *pseudomonas*  
 Q8t5j1 *Escherichia*  
 Q8t5e5 *salmonella*  
 Q8x965 *Escherichia*  
 Q8x965 *Salmonella*  
 Q8gzz *Versinia* pe  
 Q8czc *Versinia* pe  
 Q8vnr *Ralstonia* s  
 Q83sa1 *Shigella* fi  
 Q9cm70 *Pasteurella*  
 Q61164 *Plasmodium*  
 Q9576 *Chlamydomon*  
 Q7952 *bordetellla*

**RESULT 2**

Q9WWKL PRELIMINARY; PRT; 372 AA.

AC Q9WWKL;  
DT 01-NOV-1999 (TREMBLel. 12, last sequence update)  
DT 01-OCT-2003 (TREMBLel. 25, last annotation update)

DE TOLA protein.

GN OS Pseudomonas putida.

BACTERIA: Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

NCBI\_TAXID=303;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=mt-2;

RA Rodriguez-Hervia J.J., Ramos M.I., Ramos J.,  
"The Pseudomonas putida Peptidoglycan-associated outer membrane lipoprotein (PAU) is involved in maintenance of the integrity of the cell envelope.", J. Bacteriol. 178:1699-1706(1996).

RN [2] SEQUENCE FROM N.A.

RA STRAIN=mt-2;

RA Ramos-Gonzalez I.;  
Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

RN [3] SEQUENCE FROM N.A.

RA STRAIN=mt-2;

RA Rodriguez-Hervia J.J.,  
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

RN [4] SEQUENCE FROM N.A.

RC STRAIN=mt-2;

RA MEDLINE=36422022; PubMed=8824639;

RA Rodriguez-Hervia J.J., Ramos J.,  
"Characterization of an OptU null mutant of Pseudomonas putida.", J. Bacteriol. 178:1836-1840(1996).

DR EMBL; X74218; CAB50780; 1; -.

GO: GO:0000786; C:nucleosome; IEA.

GO: GO:0005634; C:nucleus; IEA.

GO: GO:0005634; :nucleus; IEA.

GO: GO:0005677; F:DNA binding; IEA.

DR InterPro; IPR00624; HISTONEH5.

PRINTS; PR00624; HISTONEH5.

KW Complete proteome.

SQ SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;

**RESULT 4**

O8T5CB PRELIMINARY; PRT; 1866 AA.

ID O8T5CB  
AC O8T5CB;  
DT 01-JUN-2002 (TREMBLel. 21, last sequence update)  
DT 01-JUN-2002 (TREMBLel. 21, last sequence update)  
DT 01-OCT-2003 (TREMBLel. 25, last annotation update)

DE MaebL.

GN MASBL.

OS Plasmidium vivax.

NCBI\_TAXID=5855;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=Salvador;

RA Michon P., Stevens J.R., Kaneko O., Adams J.H.,  
"Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites.", Mol. Biol. Evol. 0:0-0 (2002).

RT RNL; AY012083; AL010508; 1; -.

DR InterPro; IPR008602; Duffy\_binding.

DR Pfam; PF05424; Duffy\_binding; 1.

SQ SEQUENCE 1866 AA; 212420 MW; DC692D7CFAB7D93F CRC64;

Query Match 36.7%; Score 190.5; DB 5; Length 1866;

Best Local Similarity 49.6%; Pred. No. 4.1e-05;

Matches 61; Conservative 17; Mismatches 22; Indels 23; Gaps 6;

Db 177 KKAEEAKKCAEDKKKAEEAKKKAEDAKKKAAEAKKKAAADA 233

RESULT 3

Q8BN16 PRELIMINARY; PRT; 372 AA.

AC Q8BN16;  
DT 08N16;  
DT 01-JUN-2003 (TREMBLel. 24, Created)  
DT 01-JUN-2003 (TREMBLel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLel. 25, Last annotation update)

DE Biopolymer transport protein TOLA.

GN OS TOLA OR PP1221.

Pseudomonas putida (strain KT2440).



DD 178 AAAEKQKREAAKKKAEEAEEAKKAADKKAAEKAEEKA 232  
 RESULT 8 PRELIMINARY; PRT; 376 AA.  
 ID 08Z8C1; O8Z8C1;  
 AC 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2003 (TREMBLrel. 20, Last sequence update)  
 DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 TOLA protein.  
 GN STM0793 OR TOLA OR T2129.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 RN NCBI\_TaxID=601;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
 RA Baker S., Basham D., Brookes K., Chillingworth T., Connerton P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gara P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:23-52(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TY2 / ATCC 700931;  
 RX MEDLINE=2531367; PubMed=12644504;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burland V., Kotodaiami V., Schwartz D.C., Blattner F.R.;  
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
 and CT18.";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 DR EMBL; AL657268; CAD05209; 1; -;  
 DR EMBL; AE015841; AE09743; 1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 376 AA; 38804 MW; EC21F2C476ABA42 CRC64;

Query Match 34.3%; Score 178; DB 16; Length 388;  
 Best Local Similarity 52.1%; Pred. No. 6 8e-05;  
 Matches 63; Conservative 12; Mismatches 28; Indels 18; gaps 7;

QY 2 KKKAKKAEEAKKAKAKKEK----AYAKKEA-KAYKA-AEAKKAKAAKKAKAA 53  
 Db 140 KQAKAQOKIAAAKAVAKAKEBOQCRETAQAKAKBDAKIVKAQEAQKKAEEAKKAAVA 199  
 QY 54 AKAKKEAKAEEAKKAKAKKEK----AYAKKEA-AEAKKAKAAKEA 105  
 Db 200 AAQKQA-DADAKKAVEAEKAADAEEKKAAADAE-KKAALAKVAAAEAKKAAEA 257  
 QY 106 A 106  
 Db 258 A 258

RESULT 10  
 ID 08C228  
 AC 08C228;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DE Membrane spanning protein.  
 GN TOLK OR Y306.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM5 / Biolar Mediaevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Potherton J.D., Lindler L.E., Brubaker R.R., Plano G.V., Blattner F.R.,  
 RA Staley S.C., McDonough K.A., Nilles M.L., Matson J.S.,  
 RA Perry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM.";  
 RL J. Bacteriol. 184:4611-4611(2002).  
 DR EMBL; AE01306; AAM86061; -;  
 SQ SEQUENCE 393 AA; 41012 MW; 1E3E4FF878533481 CRC64;

Query Match 34.3%; Score 178; DB 16; Length 393;  
 Best Local Similarity 52.1%; Pred. No. 6 9e-05;  
 Matches 63; Conservative 12; Mismatches 28; Indels 18; gaps 7;

QY 2 KKKAKKAEEAKKAKAKKEK----AYAKKEA-KAYKA-AEAKKAKAAKKAKAA 53  
 Db 145 KQAKAQOKIAAAKAVAKAKEBOQCRETAQAKAKBDAKIVKAQEAQKKAEEAKKAAVA 204  
 QY 54 AKAKKEAKAEEAKKAKAKKEK----AYAKKEA-AEAKKAKAAKEA 105  
 Db 205 AAQKQA-DADAKKAVEAEKAADAEEKKAAADAE-KKAALAKVAAAEAKKAAEA 262

RESULT 11			
QBXVNT	PRELIMINARY;	PRT;	200 AA.
ID QBXVNT7;			
AC			
DT 01-MAR-2002 (TREMBLrel. 20, Created)			
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Probable histone H1 protein.			
GN RSC2193 OR RS00053.			
OS <i>Ralstonia solanacearum</i> (Pseudomonas solanacearum)			
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC Burkholderiaceae; Ralstonia.			
NCBI_TaxID:305;			
OX			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=GMI0001;			
RX MEDLINE=21681879; PubMed=11823852;			
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,			
RA Atilat M., Billault A., Brottier P., Camus J.C., Cattolico L.,			
RA Chandler M., Choisne N., Claude-Renard C., Gunnar S., Demange N.,			
RA Gaspin C., Lavié M., Moisan A., Robert C., Saurin W., Schlech T.,			
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,			
RT Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen <i>Ralstonia solanacearum</i> .";			
RL Nature 415:497-502 (2002).			
DR EMBL; AL64071; CAD65001; --.			
DR GO; GO:0000786; C:nucleosome; IEA.			
DR GO; GO:000534; C:nucleus; IEA.			
DR GO; GO:000577; P:DNA binding; IEA.			
DR GO; GO:000334; P:nucleosome assembly; IEA.			
DR InterPro; IPR00519; Histone_H5.			
DR PRINTS; PR00624; HISTONEH5.			
KW Complete proteome.			
SQ SEQUENCE 200 AA; 19279 MW; D3831B590510272D CRC64;			
Query Match 34.0%; Score 176.5; DB 16; Length 200;			
Best Local Similarity 54.5%; Pred. No. 4.7e-05;			
Matches 67; Conservative 5; Mismatches 32; Indels 19; Gaps 8;			
QY 1 AKKYAKKAKEYAKAKKAAKE--KAYAKYEKAYAKKAEEK--KKA---KAEKKY- 49			
Db 42 AKKVA--AKKVAKKAPEAKKAQKVAQKKAQAKAVKVAQKKAQAKAVKVVA 99			
QY 50 AKKAKAKKAKKA 106			
Db 100 AKKAAKKAQKAKVKAQKKAQAKA--APAAKKAQAKKAQAKA 156			
QY 107 YEA 109			
Db 157 KKA 159			
RESULT 12			
Q83SA1 PRELIMINARY; PRT; 413 AA.			
ID Q83SA1;			
AC			
DT 01-JUN-2003 (TREMBLrel. 24, Created)			
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Membrane spanning protein, required for outer membrane integrity.			
GN TOLA OR SF0558 OR S0571.			
OS Shigella flexneri.			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC Enterobacteriaceae; Shigella.			
NCBI_TaxID:623;			
QY [1] SEQUENCE FROM N.A.			
RP STRAIN=301 / Serotype 2a;			
RESULT 13			
Q9RM70 PRELIMINARY; PRT; 389 AA.			
ID Q9RM70			
AC			
DT 09CM70;			
DT 01-JUN-2001 (TREMBLrel. 17, Created)			
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE TOLA			
GN TOLA OR PM0368.			
OS Pasteurellamultocida.			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC Pasteurellaceae; Pasteurella.			
OX NCBI_TaxID:747;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC			
RX MEDLINE=2115866; PubMed=11246100;			
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;			
RT "Complete genomic sequence of <i>Pasteurella multocida</i> Pm70.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).			
DR EMBL; AB006125; AAK03025.1;			
DR HSP; P1994; ITOL.			
DR InterPro; IPR000533; Tropomyosin.			
DR PRINTS; PR00194; TROPOMYOSIN.			
KW Complete proteome.			
SQ SEQUENCE 389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;			
Query Match 33.4%; Score 173.5; DB 16; Length 389;			
Best Local Similarity 48.7%; Pred. No. 0.00014;			
Matches 55; Conservative 18; Mismatches 31; Indels 9; Gaps 4;			
QY 6 KRAEKAKKAKAKEYAKKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKA 56			
Db 145 KOKEAKAKQAKAKEYAKKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKA 204			



OM protein - protein search, using sw model  
Run on: April 20, 2004, 23:08:29 ; Search time 70.7792 Seconds  
Copyright (c) 1993 - 2004 Compugen Ltd.  
Title: US-009-816-989A-7  
Perfect score: 519  
Sequence: 1 AKKYYAKKAEEKAYAKKAKA. .... AKAYKAEEAKAAKEAAYEA 109  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : A\_Geneseq\_29Jan04:  
1: geneseqGP180B:/\*  
2: geneseqGP1990B:/\*  
3: geneseqGP2000S:/\*  
4: geneseqGP2001S:/\*  
5: geneseqGP2002S:/\*  
6: geneseqGP2003as:/\*  
7: geneseqGP2003bs:/\*  
8: geneseqGP2004S:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	519	100	0	AAY82577	
2	312.5	60	2	AAY82576	Ray82577 Copolymer
3	289	55	7	AAY82575	Ray82575 Copolymer
4	228.5	44	0	AAY82574	Ray82577 copolymer
5	209	40	3	AAR06415	Aar06445 Recombin
6	190.5	36	7	AABU40185	Abu40185 Protein
7	190	36	6	AABU7724	Abu7724 Protein
8	189.5	36	5	ABU28559	Abu28559 Protein
9	187	36	0	AAR06416	Aar06446 Recombin
10	184.5	35	5	ABU47123	Abu47123 Protein
11	181.5	35	0	ABU3137	Abu31397 Protein
12	180.5	34	8	AAY82573	Ray82573 Copolymer
13	179.5	34	6	AAY82499	Ray82499 Peptidom
14	179.5	34	6	AAY59044	Ray59044 Amino acid
15	179.5	34	6	AAB45852	Aab45852 Nucleicacid
16	179.5	34	6	AAU04299	Aau04289 Poly-Lys
17	179	34	5	ABU38313	Abu38313 Protein
18	179	34	5	ABJ18771	Abj18771 Pseudopeptid
19	178	34	3	AAY14928	Ray14928 Amino acid
20	178	34	3	ABP70933	Abp7093 Mycoprotein
21	178	34	3	ABU47849	Abu4784 protein
22	178	34	3	ABU50266	Abu50266 Protein
23	174	33	5	ABU44721	Abu44721 Protein
24	173.5	33	4	ABU19221	Abu19221 Protein
25	163.5	31	5	ABU17340	Abu17340 Protein

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26	163	31.4	336	6	ABU42038	Protein e	
27	162.5	31.3	543	2	ABR4568	Aarr568 Trypanoso	
28	162	31.2	356	5	ABU49418	Protein e	
29	162	31.2	356	7	ABO23526	Abro23526 Vibrio ch	
30	161	31.0	357	9	ABM67869	Abm67869 Phototrophab	
31	160.5	30.9	158	2	AYX34068	AYX34068 Histone H	
32	160.5	30.9	158	2	AYX5756	AYX5756 Human his	
33	160.5	30.9	226	2	AYX34060	AYX34060 Human his	
34	160.5	30.9	226	2	AYX7358	AYX7358 Human his	
35	160.5	30.9	468	6	ADJ35034	Adaj35034 Acinetoba	
36	160	30.8	214	6	ADJ33882	Adaj33882 Acinetobac	
37	159.5	30.7	234	5	ARH0944	Arh0944 Human lin	
38	159.5	30.7	234	7	ADD22892	Add22892 Human his	
39	159.5	30.7	472	7	ADP24569	Adp24569 Trypanoso	
40	158.5	30.5	218	2	AWM29477	Awm29477 Human his	
41	158	30.4	218	2	AYX34034	AYX34034 Human his	
42	158	30.4	218	2	AYP57332	Ayp57332 Human his	
43	157.5	30.3	564	2	ABR84565	Abra84565 Trypanoso	
44	157.5	30.3	29.8	130	5	AAB13237	Aab13237 Human lin
ALIGNMENTS							
RESULT 1							
AYX82577							
XX	AYX82577 standard; peptide, 109 AA.						
AC							
XX							
DT	28-JUL-2000 (first entry)						
XX							
DE	Copolymer molecular weight marker amino acid sequence SEQ ID NO:7.						
XX							
KW	Copolymer; molecular weight marker; TV-marker; immune disease;						
KW	glatiramer acetate; autoimmune disease; antiarthritic; antinflammatory;						
KW	osteopathic; immunosuppressive; artrhyroid; antiinflammatory;						
KW	antidiabetic; thiomimetic; haemostatic; antipsoriatic; dermatological;						
KW	antiandemic; immunosuppressive; demyelinating disease; osteoarthritis;						
KW	inflammatory condition; multiple sclerosis; rheumatoid arthritis;						
KW	Crohn's disease; chronic immune thrombocytopenia purpura; colitis;						
KW	diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;						
KW	Hachimoto's disease; idiopathic myopathy; myasthenia gravis;						
KW	pemphigus vulgaris; systemic lupus erythematosus.						
OS	Unidentified.						
XX							
PN	WO200018794-A1.						
XX							
PD	06-APR-2000.						
XX							
PF	24-SEP-1999; 99W0-US022402.						
XX							
PR	25-SEP-1998; 98US-0101693P.						
XX							
PA	(YEDA ) YEDA RES & DEV CO LTD.						
PA	(TEVA ) TEVA PHARM USA INC.						
XX							
PI	Gad A, Lis D;						
XX							
DR	WPI; 2000-317499/27.						
XX							
CC	Copolymer 1 related polypeptides used as molecular weight markers for						
CC	weight TV-marker polypeptides from the present invention. The present						
CC	invention describes polypeptides (I) for determining the molecular weight						
CC	of a copolymer (CP), which has an identified molecular weight and an						
CC	amino acid composition corresponding to the copolymer. The polypeptides						
CC	Claim 10, Page 14; 72pp; English.						

of the invention are used as molecular weight markers for glatiramer acetate related terpolymers. The polyureptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune disease which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune porphyria, autoimmune thyroiditis, autoimmune ulcerocititis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers.

ry Match 100.0%; Score 519; DB 3; Length 109;  
t local Similarity 100.0%; Pred. No. 2.9e-36;  
ches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1	AKKYAKKA YAKKAKA KEKKY YAKKEAK YAKKA EAKKK YAKKEAK KEKA	60
1	AKKYAKKA YAKKA EAKKK YAKKEAK YAKKA EAKKK YAKKEAK KEKA	60

61 YKAEEKKYAKKAKAEEKKYAAEAKKAEEAKAATKHEAANKAAGKAAYEA 109  
61 YKAEEKKYAKKAKAEEKKYAAEAKKAEEAKAATKHEAANKAAGKAAYEA 109

AAV2576 standard; peptide; 86 AA.

28-JUL-2000 (first entry)  
Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

COPOLYMER; molecular weight marker; TV-marker; immune disease; glianamer; acetate; autoimmune disease; antiarrhythmic; neuroprotective;

antidiabetic; immunosuppressive; anticholinergic; antihistaminic; antiinflammatory; antidiabetic; immunosuppressive; anticholinergic; antihistaminic; antiinflammatory; dermatological; antidiabetic; immunosuppressive; anticholinergic; antihistaminic; antiinflammatory; antidiabetic; immunosuppressive; demulcent; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; scleroderma; rheumatoid arthritis; immunosuppressive; demulcent; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; scleroderma; rheumatoid arthritis;

Crohn's disease; chronic immune thrombocytopenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barré syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;

*Unidentified.*

WO200018794-A1.  
06-APR-2000.

24-SEP-1999; 99W0-US022402.  
25-SEP-1998; 98US-0101693P.

(YEDA ) YEDA RES & DEV CO LTD.  
(TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;  
WPI; 2000-317499/27.

Copolymer 1 related polyptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

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AA1823/1 to AA1823/7 represent

invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an

amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glycoproteins or acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases

which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating

diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, autoimmune

arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's

disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's

syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-

mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease and delayed-type hypersensitivity. The

polypeptides of the invention have defined molecular weights and physical

Properties which are analogous to glutaraldehyde molecules, which makes them ideal for use as molecular weight markers

Query Match Similarity: 60.2%; Score: 312.5; DB 3; Length 86;  
 Best Local Similarity: 72.1%; Pred. No.: 3.9e-19; T=3.77

PA	(TEVA-)	TEVA PHARM USA INC.	XX
PI	Gad A,	Lis D;	PD
XX			XX
WPI:	2000-317499/27.		PP
DR			XX
PT	copolymer 1 related polypeptides used as molecular weight markers for		PR
XX	glatiramer acetate and for treatment and prevention of immune diseases.		XX
PS	Claim 10, Page 14, 72pp; English.		PA
XX			(TEVA-)
CC	AY82571 to AY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which have an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophthalmitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers sequence 77 AA;	XX	
CC	Query Match 55.7%; Score 289; DB 3; length 77; Best Local Similarity 67.0%; Pred. No. 3_1e-17; Mismatches 1; Indels 0; Gaps 0; Matches 73; Conservative 1; MisMatches 3; IndelB 32; Gaps 4; CC	AY82571 to AY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophthalmitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers sequence 77 AA;	XX
Oy	1 AKKYAKKAEKAKKAKAEEKKKYAAKKEAKKAKA 60	AY82571 to AY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophthalmitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers sequence 77 AA;	XX
Db	1 AKKYAKK-EKAYAKKA----EKA-KCA-EAKAKKA 36	AY82571 to AY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophthalmitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers sequence 77 AA;	XX
Oy	61 YKREAKKYAKAKAEEKKEYYAEEAKKA-YKA-KAKKA 109	AY82571 to AY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophthalmitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers sequence 77 AA;	XX
Db	37 -KREAKKYAKAKA-EKE-YAA-EAK-----YKA-KAKKA 77	AY82571 to AY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophthalmitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers sequence 77 AA;	XX
RESULT 4			XX
AY82574			XX
ID	AY82574 standard; peptide: 66 AA.		XX
XX			XX
AC	AY82574;		XX
XX			XX
DT	28-JUL-2000 (first entry)		XX
DE	Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.		XX
XX			XX
KW	copolymer; molecular weight marker; TV-marker; immune disease; osteopatric; autoimmune disease; antiarthritic; neuroprotective; anti-diabetic; immunosuppressive; antithyroid; antiinflammatory; anti-anaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.		XX
XX			XX
OS	Unidentified.		XX
PN	WO200018794-A1.		XX





compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one cDNA of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

Query Match 36.5%; Score 189.5; DB 6; Length 421;  
 Best Local Similarity 53.0%; Pred. No. 3.7e-08;  
 Matches 61; Conservative 11; Mismatches 32; Indels 11; Gaps 5  
 Qy 1 AKKYAKKAE---KAYAKKAKAEEKKAKYAKKEAKYAKKAEEAKYAK-TAAK 55  
 :::::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 120 ABEAKQAEELQKQAEAAKKAADAKAKAEDAKA--AEEAKKAADAKKAEDAK 177  
 :::::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Qy 56 AKKEY-KAAKUKYAKKAKEKKYAAEAKK--AEEAKYAKKAAGAAKEA 106  
 :::::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 178 AAAEAKKAKAEEAAAKKKAEEAEEAABRKKATEAEKAKAEEAKKAEEAKA 232

RESCUE  
RESULT 9  
AR0646  
AAR06446 standard; protein; 106 AA.  
AAR06446;  
25-MAR-2003 (revised)  
03-JAN-1991 (first entry)  
Recombinant copolymer 1-19, myelin basic protein analogue.  
Recombinant Copolymer 1; COP-1-19; myelin basic protein; MBP;  
immunological activity; autoimmune encephalomyelitis; multiple sclerosis.  
Synthetic.  
EP3836220-A.  
22-AUG-1990.  
16-FEB-1990; 90EP-00301700.  
17-FEB-1989; 89US-00312541.  
07-FEB-1990; 90US-00413845.  
(REPK) REPLIGEN CORP.  
Cook RS;  
WPI; 1990-255840/34.  
N-PSDB; ARQ06446.  
Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.  
Disclosure; Fig 12; 25pp; English.

CC

polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

Sequence 407 AA:  
**RESULT 11**  
 ABU1397  
 ID ABU1397 standard; protein; 323 AA.  
 XX  
 AC ABU1397;  
 XX  
 DT 19-JUN-2003 (first entry)  
 DE Protein encoded by prokaryotic essential gene #16924.  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 OS Klebsiella pneumoniae.  
 XX  
 WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PP 21-MAR-2002; 2002W0-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00348993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
 Wall D, Trawick JD, Carr GA, Yamamoto R, Forsyth RA, Xu HH;  
 DR WPI; 2003-029926/02.

DR N-PSDB; ACA35267.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX PT Claim 25; SEQ ID NO 59321; 176PP; English.

XX PS

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

SQ

Sequence 323 AA:  
**RESULT 12**  
 AY82573  
 ID AY82573 standard; peptide; 56 AA.  
 XX  
 AC AY82573;  
 XX  
 PR 28-JUL-2000 (first entry)  
 XX  
 DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.  
 XX  
 PR Copolymer; molecular weight marker; TV-marker; immune disease; KW glatiramer acetate; autoimmune disease; antiarthritis; neuroprotective; KW osteopathic; immunosuppressive; antithyroid; antiinflammatory; KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; KW antiamebic; immunosuppressive; demyelinating disease; osteoarthritis; KW inflammatory condition; multiple sclerosis; rheumatoid arthritis; KW Crohn's disease; chronic immune thrombocytopenia; colitis; KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;





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OM protein - protein search, using sw model  
Run on: April 20, 2004, 23:17:50 ; Search time 53.7922 Seconds  
Perfect score: US-09-816-989A-7  
Sequence: 519 AKYVAKKAEKAYAKKAKA.....AKAVGKEARKAAKEAYEA 109  
Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues  
Total number of hits satisfying chosen parameters: 1124875  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications-AA.\*  
1: /cgn2\_6/podata/1/pubaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/podata/1/pubaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/podata/1/pubaa/US06\_NEW\_PUB.pep:\*
4: /cgn2\_6/podata/1/pubaa/US06\_PUBCOMB.pep:\*
5: /cgn2\_6/podata/1/pubaa/US07\_NEW\_PUB.pep:\*
6: /cgn2\_6/podata/1/pubaa/PCTUS\_PUBCOMB.pep:\*
7: /cgn2\_6/podata/1/pubaa/US08\_NEW\_PUB.pep:\*
8: /cgn2\_6/podata/1/pubaa/US09A\_PUBCOMB.pep:\*
9: /cgn2\_6/podata/1/pubaa/US09B\_PUBCOMB.pep:\*
10: /cgn2\_6/podata/1/pubaa/US09C\_PUBCOMB.pep:\*
11: /cgn2\_6/podata/1/pubaa/US10A\_PUBCOMB.pep:\*
12: /cgn2\_6/podata/1/pubaa/US10B\_PUBCOMB.pep:\*
13: /cgn2\_6/podata/1/pubaa/US10B\_PUBCOMB.pep:\*
14: /cgn2\_6/podata/1/pubaa/US10C\_PUBCOMB.pep:\*
15: /cgn2\_6/podata/1/pubaa/US10C\_PUBCOMB.pep:\*
16: /cgn2\_6/podata/1/pubaa/US60\_NEW\_PUB.pep:\*
17: /cgn2\_6/podata/1/pubaa/US60\_PUBCOMB.pep:\*
18: /cgn2\_6/podata/1/pubaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	519	100.0	109	9 US-09-816-989A-7 Sequence 7, Appli
2	312.5	60.2	86	9 US-09-816-989A-7 Sequence 6, Appli
3	289	55.7	77	9 US-09-816-989A-7 Sequence 5, Appli
4	228.5	44.0	66	9 US-09-816-989A-4 Sequence 4, Appli
5	190.5	36.7	372	12 US-10-202-122A-68109 Sequence 63109, A
6	190	36.5	428	12 US-10-202-122A-55748 Sequence 53748, A
7	189.5	36.5	421	12 US-10-202-122A-56483 Sequence 5483, A
8	184.5	35.5	407	12 US-10-202-122A-75047 Sequence 75047, A
9	181.5	35.0	323	12 US-10-202-122A-5921 Sequence 5321, A
10	180.5	34.8	56	9 US-09-816-989A-3 Sequence 3, Appli
11	179	34.5	347	12 US-10-282-122A-66237 Sequence 6237, A
12	179	34.5	347	12 US-10-127-032-120 Sequence 120, App
13	178	34.3	223	13 US-10-051-63-201 Sequence 201, App
14	178	34.3	223	14 US-10-105-97-5 Sequence 52, Appli
15	178	34.3	376	12 US-10-202-122A-75772 Sequence 75772, A

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Match	Length	DB	IB	Description
1	519	100-0	109	9	US-09-816-989A-7	Sequence 7, Appli
2	312.5	60-2	86	9	US-09-816-989A-6	Sequence 6, Appli
3	289	55-7	77	9	US-09-816-989A-5	Sequence 5, Appli
4	228.5	44-0	66	9	US-09-816-989A-4	Sequence 4, Appli
5	190.5	36-7	372	12	US-10-282-122A-8109	Sequence 68109,
6	190	36-6	428	12	US-10-282-122A-5748	Sequence 55748,
7	189.5	36-5	421	12	US-10-282-122A-5483	Sequence 5483,
8	184.5	35-5	407	12	US-10-282-122A-5047	Sequence 75047,
9	181.5	35-0	323	12	US-10-282-122A-59321	Sequence 59321,
10	180.5	34-8	56	9	US-09-816-989A-3	Sequence 3, Appli
11	179	34-5	347	12	US-10-282-122A-66237	Sequence 66237,
12	179	34-5	347	14	US-10-127-032-120	Sequence 120, AP
13	178	34-3	223	13	US-10-051-643-201	Sequence 201, AP
14	178	34-3	223	14	US-10-205-979-52	Sequence 52, AP
15	178	34-3	376	12	US-10-282-122A-5772	Sequence 75772,

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 2  
US-09-816-989A-6  
; Sequence 6, Application US/09816989A  
; Patent No. US20020115103A1

; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; L1s, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK  
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE  
; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816,989A  
; CURRENT FILING DATE: 2001-03-23  
; PRIORITY FILING DATE: 1998-09-25  
; PRIORITY APPLICATION NUMBER: PCT/US99/22402  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-6

Query Match Best Local Similarity 60.2%; Score 312.5; DB 9; Length 86;  
Matches 80; Conservative 1; Mismatches 3; Indels 27; Gaps 5;  
Qy 1 AKKYAKKAKAKKAEEKEYAAEAK-KAAKKAEEAKKAKKAEEAKKAAYEA 60  
Db 1 AKKYAKK-EKAYAKKA---EKA-KKA-EKAYAKKA-EAKKA--- 36

Qy 61 YKA-EAKKAKAKKAEEKEYAAEAK-KAAKKAEEAKKAKKAEEAKKAAYEA 109  
Db 37 -KA-EAKKAKAKKAEEKEYAAEAK-KAAKKAEEAKKAAYEA 86

RESULT 3  
US-09-816-989A-5  
; Sequence 5, Application US/09816989A  
; Patent No. US20020115103A1

; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; L1s, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK  
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE  
; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816,989A  
; CURRENT FILING DATE: 2001-03-23  
; PRIORITY APPLICATION NUMBER: 60/101,693  
; PRIORITY FILING DATE: 1998-09-25  
; PRIORITY APPLICATION NUMBER: PCT/US99/22402  
; PRIORITY FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-4

Query Match Best Local Similarity 44.0%; Score 228.5; DB 9; Length 66;  
Matches 62; Conservative 0; Mismatches 4; Indels 43; Gaps 4;  
Qy 1 AKKYAKKAKAKKAEEKEYAAEAK-KAAKKAEEAKKAKKAEEAKKAAYEA 60  
Db 1 AKKYAKK-EKAYAKKA---EAKAKKA---EAKAKKA--- 25

Qy 61 YKA-EAKKAKAKKAEEKEYAAEAK-KAAKKAEEAKKAKKAEEAKKAAYEA 109  
Do 26 -KA-EAKKAKAKKAEEKEYAAEAK---YKA-EAKKAAYEA 66

RESULT 5  
US-10-282-122A-68109  
; Sequence 68109, Application US/10282122A  
; Publication No. US20040029129A1

; GENERAL INFORMATION:  
; APPLICANT: Wang, Liansu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haslebeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: EULTRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIORITY APPLICATION NUMBER: 60/191,078  
; PRIORITY FILING DATE: 2000-03-21  
; PRIORITY APPLICATION NUMBER: 60/206,848  
; PRIORITY FILING DATE: 2000-05-23  
; PRIORITY APPLICATION NUMBER: 60/207,727  
; PRIORITY FILING DATE: 2000-05-26  
; PRIORITY APPLICATION NUMBER: 60/230,335

Query Match Best Local Similarity 55.7%; Score 289; DB 9; Length 77;  
Matches 73; Conservative 1; Mismatches 3; Indels 32; Gaps 4;  
Qy 1 AKKYAKKAKAKKAEEKEYAAEAK-KAAKKAEEAKKAKKAEEAKKAAYEA 60  
Db 1 AKKYAKK-EKAYAKKA---EKA-KKA-EAKKAAYEA 36



SEQ ID NO 56483 ;  
 LENGTH: 421 ;  
 TYPE: PRT ;  
 ORGANISM: Escherichia coli  
 US-10-282-12A-56483

Query Match 36.5%; Score 189.5; DB 12; Length 421;  
 Best Local Similarity 53.0%; Pred. No. 1.2e-07; Mismatches 61; Conservatve 11; Mismatches 32; Indels 11; Gaps 5; Matches 61;

Qy 1 AKKYAKKAE---KAYAKKAKEKKAKYAAEKKYAK-EAKK 55  
 Db 120 AEEAKQAKELQKQAAEAAKAKAAEADKA--AEEAKGAAADAKKAEEAK 177

Qy 56 AKKEAY-KAEKYAKAAKAEKEYAAEAKK--ABAKAYKAAKAAKAYEA 106  
 Db 178 AAAEAKQKAAEAAAKKCAAAEAAEAAEAKRAKAAKAAEAKA 232

RESULT 8  
 US-10-282-122A-75047  
 Sequence 75047, Application US/10282122A  
 Publication No. US200404029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Haseelbeck, Robert  
 APPLICANT: Olsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forbyth, R.  
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282.122A

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 7614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 59321

LENGTH: 323

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-10-282-122A-59321

Query Match 35.0%; Score 181.5; DB 12; Length 323;  
 Best Local Similarity 52.7%; Pred. No. 4.1e-07; Mismatches 59; Conservatve 8; MisMatches 34; Indels 11; Gaps 4; Matches 66; Conservatve 11; Mismatches 25; Indels 17; Gaps 8; LENGTH: 407

Qy 1 AKKYAKKAKYAAKAKAEKEYAAEAKKAAEAKYAK-EAKK 55  
 Db 47 ADAOKAAQAAAGAAADIK-KOEA--AAKAAEAKQAAEAKAAEQQKCAA 102

Qy 56 -AKKEAYKLEAKYAKAAKAEKEYAAEAKKAAEAKYAK-EAKK 106  
 Db 103 AAQKAQAEKQAAQEAQKQAAEKAQAAEKAQAAEKAQAAEKA 153

Query Match 35.5%; Score 184.5; DB 12; Length 407;  
 Best Local Similarity 55.5%; Pred. No. 3e-07; Mismatches 66; Conservatve 11; Mismatches 25; Indels 17; Gaps 8; LENGTH: 407

Qy ORGANISM: Salmonella typhimurium

US-10-282-122A-75047

Query Match 35.5%; Score 184.5; DB 12; Length 407;  
 Best Local Similarity 55.5%; Pred. No. 3e-07; Mismatches 66; Conservatve 11; Mismatches 25; Indels 17; Gaps 8; LENGTH: 407

Qy ORGANISM: Escherichia coli

US-10-282-12A-56483

Query Match 36.5%; Score 189.5; DB 12; Length 421;  
 Best Local Similarity 53.0%; Pred. No. 1.2e-07; Mismatches 61; Conservatve 11; MisMatches 32; Indels 11; Gaps 5; Matches 61;

Qy 1 AKKYAKKAE---KAYAKKAKEKKAKYAAEKKYAK-EAKK 55  
 Db 120 AEEAKQAKELQKQAAEAAKAKAAEADKA--AEEAKGAAADAKKAEEAK 177

Qy 59 EAKY--AEAKYAKAAKAKYAAEAKK--AEAKYKAK--AAEAKAYEA 109  
 Db 196 EAKAAEAKKAAEAK---AAEAKKAADEAAKA-AAAKKAADAAKAAA 249

RESULT 9  
 US-10-282-122A-59321  
 Sequence 59321, Application US/10282122A  
 Publication No. US200404029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Olsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Travick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forbyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282.122A

CURRENT FILING DATE: 2003-07-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 7614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 59321

LENGTH: 323

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-10-282-122A-59321



APPLICANT: Tan, Paul L. J.  
 TITLE OF INVENTION: Methods and Compounds for the Treatment of Immunologically-Mediated Diseases of the Respiratory System using Mycobacterium Vaccae  
 TITLE OF INVENTION: System using Mycobacterium Vaccae  
 FILE REFERENCE: 11000-1008c2  
 CURRENT APPLICATION NUMBER: US/10/051,643  
 CURRENT FILING DATE: 2002-01-18  
 PRIOR APPLICATION NUMBER: US09/156,181  
 PRIOR FILING DATE: 1998-09-17  
 PRIOR APPLICATION NUMBER: US 08/996,624  
 PRIOR FILING DATE: 1997-12-23  
 NUMBER OF SEQ ID NOS: 208  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 201  
 LENGTH: 223  
 TYPE: PRT  
 ORGANISM: Mycobacterium vaccae  
 US-10-051-643-201  
 Query Match 34.3%; Score 178; DB 13; Length 223;  
 Best Local Similarity 54.5%; Pred. No. 5.2e-07;  
 Matches 60; Conservative 6; Mismatches 34; Indels 10; Gaps 5;  
 QY 1 AKKYAKK--AEKYAKKAKA  
 Db 112 ARKAAGKAPAKGAAKQAPAKKAPAK  
 QY 56 AKKEAYKAEAKKYAKA  
 Db 171 AKKAPAKKAATKAPAKKAATKAPAKKAPAK--KAPAKKAPAK 218  
 RESULT 14  
 US-10-205-979-52  
 ; Sequence 52, Application US/10205979  
 ; GENERAL INFORMATION:  
 ; Publication No. US20030147861A1  
 ; APPLICANT: Watson, James D.  
 ; APPLICANT: Tan, Paul L. J.  
 ; APPLICANT: Abernethy, Nevin  
 ; TITLE OF INVENTION: Compounds and Methods for the Modulation of Immune Responses  
 ; FILE REFERENCE: 1100-1063U  
 ; CURRENT APPLICATION NUMBER: US/10/205,979  
 ; CURRENT FILING DATE: 2002-07-25  
 ; PRIOR APPLICATION NUMBER: 60/309,446  
 ; PRIOR FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SEQ ID NO 52  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: Mycobacterium vaccae  
 ; US-10-205-979-52  
 Query Match 34.3%; Score 178; DB 14; Length 223;  
 Best Local Similarity 54.5%; Pred. No. 5.2e-07;  
 Matches 60; Conservative 6; Mismatches 34; Indels 10; Gaps 5;  
 QY 1 AKKYAKK--AEKYAKKAKA  
 Db 112 ARKAAGKAPAKGAAKQAPAKKAPAK  
 QY 56 AKKEAYKAEAKKYAKA  
 Db 171 AKKAPAKKAATKAPAKKAATKAPAKKAPAK--KAPAKKAPAK 218  
 RESULT 15  
 US-10-282-122A-75772  
 ; Sequence 75772, Application US/10282122A  
 ; Publication No. US2004029129A1  
 ; GENERAL INFORMATION:

---

APPLICANT: Wang, Liangshu  
 APPLICANT: Zanudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Olsen, Kari  
 APPLICANT: Zuskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELTRA\_034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-31  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-06  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SEQ ID NO 78614  
 LENGTH: 376  
 TYPE: PRT  
 ORGANISM: Salmonella typhi  
 US-10-282-122A-75772  
 Query Match 34.3%; Score 178; DB 12; Length 376;  
 Best Local Similarity 52.3%; Pred. No. 9e-07;  
 Matches 58; Conservative 10; Mismatches 33; Indels 10; Gaps 4;  
 QY 1 AKKYAKKAKA  
 Db 137 AKKAADAKKAKA  
 QY 51 YKEAKKAKA  
 Db 191 -KAEAEAKAAADAKKKADEAKAAEAKKKADAAKAA  
 Search completed: April 20, 2004, 23:27:18  
 Job time : 54.7928cs

FILE REFERENCE: 2709\_1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIORITY FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5390  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: *Proteus mirabilis*  
; US-09-543-681A-5390

RESULT 15

Query Match 32.6%; Score 169; DB 4; Length 361;

Best Local Similarity 44.4%; Pred. No. 3.2e-07; Matches 51; Conservatve 16; Mismatches 37; Indels 12; Gaps 2;

Qy	1 AKKAKKAEEAKYAKKAKAAKEKKYAKKAKAYA-----AEAKKKAKAAKEAKYAK 51
Db	123 AKEAEAAEAEAAEAAKAKKEQOKAQAAKARDRILKEQADAKAKAAEAKQAE 182
Qy	52 EAAKKEAKYAKKAKAAEAKYAKA--AKAEECYAALEAKYAAEAKYKEAAKAAKE 104
Db	183 LAQKKAEEAKAKAAEAKKAAEAKAAEAKAAEAKAAEAKAAEAKAAEAKAAEAKAAQ 238

Qy 57 KK-EAKYKAAEAKYAKAKAAKEKYYA---AEAKKAELAKAVK-AEAKAAKEAA 106  
Db 505 TKVAEAKQRAEAETKVAAEAKQRAEAETKVAAEAKQRAEAETKVAAEAKQRAEA 561

Search completed: April 20, 2004, 23:19:08  
Job time : 23.6494 secs

US-08-216-894-8

; Sequence 8, Application US/08216894

; Patent No. 5876734

; GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Otsu, Keiko

TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/216 894

FILING DATE: 24-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REFERENCE/DOCKET NUMBER: 29\_768

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 677-5300

TELEFAX: 904136

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 643 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-216-894-8

Query Match 31.3%; Score 162.5; DB 2; Length 643;

Best Local Similarity 44.4%; Pred. No. 2e-06; Matches 52; Conservatve 18; Mismatches 36; Indels 11; Gaps 4;

Qy 1 AKKAKKAEEAKYAKKAKAAKEKKYAKKAKAYA-----AEAKKA 56

Db 445 AAATKVAEAKQAAEAKVAAEAKQAAEAKVAAEAKVAAEAKQAAEA 504







FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: Peptide  
; US-09-405-743A-6

Query Match Similarity 60.2%; Score 312.5; DB 4; Length 86;  
; Best Local Similarity 72.1%; Pred. No. 7.8e-20; Mismatches 3; Indels 43; Gaps 4;  
; Matches 80; Conservative 1; Mismatches 3; Indels 27; Gaps 5;

QY 1 AKKYAKKAKAYAKKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA 60  
; Db 1 AKKYAKKAKAYAKKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA 60  
; Db 37 -KAEAKKYAKAKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA----- 36

RESULT 3 US-09-405-743A-5  
; Sequence 5, Application US/09405743A  
; Patent No. 6514938

GENERAL INFORMATION:  
; APPLICANT: Yeda Research and Development Co., Ltd.  
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS  
; FILE REFERENCE: 60807-A  
; CURRENT APPLICATION NUMBER: US/09/405,743A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 77

ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: Peptide  
; US-09-405-743A-5

Query Match Similarity 55.7%; Score 289; DB 4; Length 77;  
; Best Local Similarity 67.0%; Pred. No. 6.4e-18; Mismatches 3; Indels 32; Gaps 4;  
; Matches 73; Conservative 1; Mismatches 3; Indels 32; Gaps 4;

Qy 1 AKKYAKKAKAYAKKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA 60  
; Db 1 AKKYAKK-EKAYAKKA---EKAKKAKAKYAKKEAKKAKA----- 36

Qy 61 YKAEEKYAKAKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA 109  
; Db 37 -KAEAKKYAKAKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA----- 77

RESULT 4 US-09-405-743A-4  
; Sequence 4, Application US/09405743A  
; Patent No. 6514938

GENERAL INFORMATION:  
; APPLICANT: Yeda Research and Development Co., Ltd.  
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS  
; FILE REFERENCE: 60807-A  
; CURRENT APPLICATION NUMBER: US/09/405,743A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 66

TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: Peptide  
; US-09-405-743A-4

RESULT 5 US-09-489-039A-13565  
; Sequence 5, Application US/09489039A  
; Patent No. 6610836

GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709, 2000-01  
; CURRENT APPLICATION NUMBER: US/09/489, 039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13965  
; LENGTH: 469

TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
; US-09-489-039A-13565

Query Match Similarity 37.8%; Score 196; DB 4; Length 469;  
; Best Local Similarity 51.2%; Pred. No. 2.3e-09; Mismatches 35; Indels 12; Gaps 4;  
; Matches 62; Conservative 12; Mismatches 35; Indels 12; Gaps 4;

Qy 1 AKKYAKKAKAYAKKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA 53  
; Db 153 AKEQOKQAAEAKAKAAKAKADQAKRQAQAKAKAAKAKADQAKAQQAAKA 212

Qy 54 AKKYAKKAKAYAKKAKAKKEKKAKYAKKEAKKAKAAKKAEEAKYKAEAKKAKA 108  
; Db 213 ADAKKQEAQAKAKAEEAKQQAEEAKAAQAKQKAEEAKQQAEEAKQQAEEAKQ 272

Qy 109 A 109  
; Db 273 A 273

RESULT 6 US-09-405-743A-3  
; Sequence 3, Application US/09405743A  
; Patent No. 6514938

GENERAL INFORMATION:  
; APPLICANT: Yeda Research and Development Co., Ltd.  
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS  
; FILE REFERENCE: 60807-A  
; CURRENT APPLICATION NUMBER: US/09/405,743A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 56

TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: Peptide  
; US-09-405-743A-3

Query Match Similarity 45.9%; Score 180.5; DB 4; Length 56;  
; Best Local Similarity 56.9%; Pred. No. 5.4e-09;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: April 20, 2004, 23:14:00 ; Search time 22.6494 Seconds  
(without alignments) 248.450 Million cell updates/sec

Title: US-09-816-989a-7

Perfect score: 519

Sequence: 1 AKKYAKKAKAKAYAKAKAAK... . . . . . AKAYKAELAKAAKEAAYEA 109

Scoring table: BiOSUM62 Gapop 10.0 , Gabext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database :

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3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB\_pep;\*  
4: /cgn2\_6/ptcdata/2/iaa/6B\_COMB\_pep;\*  
5: /cgn2\_6/ptcdata/2/iaa/PCTUS\_COMB\_pep;\*  
6: /cgn2\_5/ptcdata/2/iaa/batchfile1.pep;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match Length	DB ID	Description
1	519	100.0	109	Sequence 7, Appli
2	312.5	60.2	4	US-09-405-743A-5
3	289	55.7	77	Sequence 6, Appli
4	228.5	44.0	4	US-09-405-743A-5
5	196	37.8	4	US-09-405-743A-4
6	180.5	34.8	56	Sequence 5, Appli
7	179.5	34.6	100	US-09-405-743A-3
8	179.5	34.6	100	US-08-460-890A-64
9	179.5	34.6	100	US-08-460-971A-64
10	179.5	34.6	100	US-08-460-971A-64
11	179	34.5	407	US-08-462-940A-64
12	178	34.3	223	US-09-405-855A-201
13	178	34.3	223	US-09-405-855A-201
14	169	32.6	361	US-09-453-681A-530
15	162.5	31.3	643	US-08-216-894A-8
16	162.5	31.3	643	US-09-415-746A-8
17	160.5	30.9	158	US-09-041-881A-40
18	160.5	30.9	158	US-09-417-263A-40
19	160.5	30.9	226	US-09-041-883A-32
20	160.5	30.9	226	US-09-417-263A-32
21	160.5	30.9	468	US-09-328-312-6321
22	160	30.8	324	US-09-328-312-5169
23	158.5	30.5	472	US-08-216-894A-10
24	158.5	30.5	472	US-09-115-746A-10
25	158.5	30.5	564	US-08-216-894A-2
26	158.5	30.5	564	US-09-115-746A-2
27	158	30.4	389414	US-09-041-889A-4

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database :

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3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB\_pep;\*  
4: /cgn2\_6/ptcdata/2/iaa/6B\_COMB\_pep;\*  
5: /cgn2\_6/ptcdata/2/iaa/PCTUS\_COMB\_pep;\*  
6: /cgn2\_5/ptcdata/2/iaa/batchfile1.pep;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match Length	DB ID	Description
1	519	100.0	109	Sequence 7, Appli
2	312.5	60.2	4	US-09-405-743A-5
3	289	55.7	77	Sequence 6, Appli
4	228.5	44.0	66	US-09-405-743A-4
5	196	37.8	49	US-09-405-743A-3
6	180.5	34.8	56	Sequence 5, Appli
7	179.5	34.6	100	US-08-460-890A-64
8	179.5	34.6	100	US-08-460-971A-64
9	179.5	34.6	100	US-08-460-971A-64
10	179.5	34.6	100	US-08-460-971A-64
11	179	34.5	407	US-08-462-940A-64
12	178	34.3	223	US-09-405-855A-201
13	178	34.3	223	US-09-405-855A-201
14	169	32.6	361	US-09-453-681A-530
15	162.5	31.3	643	US-08-216-894A-8
16	162.5	31.3	643	US-09-415-746A-8
17	160.5	30.9	158	US-09-041-881A-40
18	160.5	30.9	158	US-09-417-263A-40
19	160.5	30.9	226	US-09-041-883A-32
20	160.5	30.9	226	US-09-417-263A-32
21	160.5	30.9	468	US-09-328-312-6321
22	160	30.8	324	US-09-328-312-5169
23	158.5	30.5	472	US-08-216-894A-10
24	158.5	30.5	472	US-09-115-746A-10
25	158.5	30.5	564	US-08-216-894A-2
26	158.5	30.5	564	US-09-115-746A-2
27	158	30.4	389414	US-09-041-889A-4

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database :

Issued\_Patents\_AA;\*  
1: /cgn2\_6/ptcdata/2/iaa/5A\_COMB\_pep;\*  
2: /cgn2\_6/ptcdata/2/iaa/5B\_COMB\_pep;\*  
3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB\_pep;\*  
4: /cgn2\_6/ptcdata/2/iaa/6B\_COMB\_pep;\*  
5: /cgn2\_6/ptcdata/2/iaa/PCTUS\_COMB\_pep;\*  
6: /cgn2\_5/ptcdata/2/iaa/batchfile1.pep;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match Length	DB ID	Description
1	519	100.0	109	Sequence 7, Appli
2	312.5	60.2	4	US-09-405-743A-5
3	289	55.7	77	Sequence 6, Appli
4	228.5	44.0	66	US-09-405-743A-4
5	196	37.8	49	US-09-405-743A-3
6	180.5	34.8	56	Sequence 5, Appli
7	179.5	34.6	100	US-08-460-890A-64
8	179.5	34.6	100	US-08-460-971A-64
9	179.5	34.6	100	US-08-460-971A-64
10	179.5	34.6	100	US-08-460-971A-64
11	179	34.5	407	US-08-462-940A-64
12	178	34.3	223	US-09-405-855A-201
13	178	34.3	223	US-09-405-855A-201
14	169	32.6	361	US-09-453-681A-530
15	162.5	31.3	643	US-08-216-894A-8
16	162.5	31.3	643	US-09-415-746A-8
17	160.5	30.9	158	US-09-041-881A-40
18	160.5	30.9	158	US-09-417-263A-40
19	160.5	30.9	226	US-09-041-883A-32
20	160.5	30.9	226	US-09-417-263A-32
21	160.5	30.9	468	US-09-328-312-6321
22	160	30.8	324	US-09-328-312-5169
23	158.5	30.5	472	US-08-216-894A-10
24	158.5	30.5	472	US-09-115-746A-10
25	158.5	30.5	564	US-08-216-894A-2
26	158.5	30.5	564	US-09-115-746A-2
27	158	30.4	389414	US-09-041-889A-4

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Maximum Match 100%

Listing First 45 summaries

Database :

Issued\_Patents\_AA;\*  
1: /cgn2\_6/ptcdata/2/iaa/5A\_COMB\_pep;\*  
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3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB\_pep;\*  
4: /cgn2\_6/ptcdata/2/iaa/6B\_COMB\_pep;\*  
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4	228.5	44.0	66	US-09-405-743A-4
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9	179.5	34.6	100	US-08-460-971A-64
10	179.5	34.6	100	US-08-460-971A-64
11	179	34.5	407	US-08-462-940A-64
12	178	34.3	223	US-09-405-855A-201
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Database :

Issued\_Patents\_AA;\*  
1: /cgn2\_6/ptcdata/2/iaa/5A\_COMB\_pep;\*  
2: /cgn2\_6/ptcdata/2/iaa/5B\_COMB\_pep;\*  
3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB\_pep;\*  
4: /cgn2\_6/ptcdata/2/iaa/6B\_COMB\_pep;\*  
5: /cgn2\_6/ptcdata/2/iaa/PCTUS\_COMB\_pep;\*  
6: /cgn2\_5/ptcdata/2/iaa/batchfile1.pep;\*

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#### SUMMARIES

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Result No.	Score	Query Match Length	DB ID	Description




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